ACCIOCAGAC TOTOCOGTGA ACAGATATTO GOCOCTGTGG COGTAGTTGC GAAATTCAAG	180
GACTACGATG AAGCTATTCG TTACGCTAAT GACACTAACT ATGGGCTGGC ATCCTGCGTT	240
TICACIGAAA ACATACOCOT TOCGCACCOC TITIGIOCGIG AIGICCAATC TOOCACTGIG	300
TOOGTTAATT CCTCTAATGA TGAGGAGGIG GGAGTGCCTT TTGGCGGGTT CAAGATGAGC	360
GETATOGGAA GEGAGCTOGG GAAGGCAGEC CTGCAAACTT ACCTOCAGAC TAAAGCAGTA	420
CACCTGAACT TIGCTTAGAT AGAGCAACTC ATATATTAGA ATCACTICAT ACATCAACTA	480
TATATCATTA TGIATATCAC TATOCCAGAG GIGIAGIOGA ACCACTATUT ATCACGIGAT	540
ACCOCTICCC COCTICATOCC COCCACTACCT COCTTOCACA ACCOCCCCCA CACATTICASC	600
AGGIGCIATA TACACTICIC GAGGACAGIA TOOCACOCAG TACCATTATA GCAAGIAAGC	660
CETETECTET TTOCATAAAG CETAAGETCA AGTECCACCG GCTOGTTCCC TOCACGAACT	720
GTGTCAA	727
(2) INFORMATION FOR SEQ ID NO:739:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 683 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEINESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: PAG1481RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:739:	
CATCGATAGG CCACACTTTC ATGGTTTGTA TICACACTGA AAATCAAAAT CAAGGGGACT	60
THTACCCUTT TOURCIACTE GACATUTCIC TUCIOCATGA GUCCCCCTTA GGACATOTOC	120

(II) 39h

	GITATICUTT AACAGATGTG CCCCCCCAGC CAAACTCCCCC ACCTGACAAT GTCTTCAACC	180
5	COCATCAGCC CGUATAGGAC TUTAAATOCT AGAAGGTOGA AAATGAATTC CAGCTOCGCT	240
	TAATIGAATA AGTAAAGAAA CTATAAAGGT AGTGGTATTT CACTGGCGCC GAAGCTCCCA	300
10	CITATICIAC ACCCICIATG TCTCTTCACA ATGTCAAACT AGAGTCAAGC TCAACAGGGT	360
	CITCHTICCC CGCIGATICT GCCAAGCCCG TICCCTIGGC TGIGGITTICG CTAGATAGTA	420
15	GATAGGGACA GTGGGAATCT CGTTAATCCA TTCATGCGGG TCACTAATTA GATGACGAGG	480
	CATTIGGCTA CCTTAAGAGA GICATAGTTA CICCOGCOGT TIACCOGCGC TIGGTIGAAT	540
20	TICITCACIT TGACATTCAG AGCACTGGGC AGAAATCACA TTGGGTCAAC ATCACTTTCT	600
	GACCATCOCA AUGCTATOIT TUAATUAGAC AGTCAGATUC COCTUGUCOG TACCAGUICT	660
2 5	AAGITGATOG TTAATTIGTAG CAA	683
	(2) INFORMATION FOR SEQ ID NO:740:	
3 0	(i) SEQUENCE CHARACTERISTICS:	
	(A) LEWIH: 657 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genamic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1481UP	
45		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:740:	
5 <i>0</i>	GATCOOGTICG TGTTTTCTTA TGACCCACTC GOCACCITTAC GAGAAATCAA AGTCTTTOOG	60
	TTCTGGGGGG AGTATGGTCG CAAGGCTGAA ACTTAAAGGA ATTGACGGAA GGGCACCACC	120
55	AGGAGTIGGAG CCTGCGGCTT AATTTIGACTC AACACGGGGA AACTCACCAG GTCCAGACAC	180

	AATAAGGATT GACAGATTGA GASCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCCGT	240
5	TOTTAGITIGG TOGAGTIGATT TGTOTOCTTA ATTICOGATAA CGAACGAGAC CTTAACCTAC	300
	TARATACTOC TOCTAGCATT TOCTOCTTCC GCACTTCTTA GAGGGACTAT CGGTTTCAAG	360
10	CCGATGGAAG TTTGAGGCAA TAACAGGTCT GTGATGCCCT TAGACGTTCT GGGCCGCACG	420
	COCCCTACAC TGACGGAGCC AGCGAGTATA ACCTTGCCCG AGAGGTCTGG GTAATCTTGT	480
15	GAAACTCCGT CGTGCTGGGG ATAGAGCATT GCAATTATTG CTCTTCAACG AGGAATTCCT	540
	AGTAAGOGCA AGTCATCAGC TTGOGTTGAT TAOGTCCCTG CCCTTTGTAC ACACCGCCCG	600
20	TOGOTAGIAC OGATICAATG GCITAGIGAG GCCTCAGGAT CIGCITAGAG GAGGGGG	657
	(2) INFORMATION FOR SEQ ID NO:741:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 694 base pairs (B) TYPE: nucleic acid	
30	(C) STRANDELNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1482RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:741:	
45	GATCCATTCG TTAATATGCA TIGTCTACAG TGAGAGCAAA GAGGGCGGG GATTTAAAGC	60
	ATGGTGGGGC GACGCCTATT TTAAATGGGG GITGITTIGCA ACGGTTTTIGG CCGGGCTTCT	120
50	TOTOCTOCAT AGTGAAAAGT TCATTCGCCA AAGAACGTAC GAATTCTTTC TGATACTGCA	180
	CAAGCTOTTC AACATTGTCT TTATTGTATG CATGTATATG CACATCAAAA COCTGGGATG	240
55	OCACOOCTOG GTCTOGTOGA TOGTTOCCAT CTACTOCTTC GAGOGTGTOG OCCOGGATAGC	300

	ICOCALIGIA CITULIOCAG GCATCAAGAA GGCCACATTA ACAGATGITG GGCATCCCGT	360
5	OCTCAAGATG ACAGTOGAGA AGOCAAAGCA TTICAAATAT TACOCGOGG CTTATGTTTT	420
	CGITTATTIT ATTAGTOOGA AGGATOCTIG GITCIATCCA TICCAGTOGC ACCOGNICAC	480
10	CGICCTTAAT ACACCCAAGA TOGATOGOGA CAACCTGGTG ATTTATTTCA AAGTOCACAA	540
	GOGCGIGACG CAGCAGCTGC TAAACAGGAT CTTTCTATCC GGGAAAGAGT CCATCGAATA	600
15	CAAGGIGCTT CIAGAAGGGC CCTATGCAAA CACCATTGCG CGCCTTGCTG CTCCTGACCG	660
	GOGCTACGIG GGCGCCAGCG CACGICTICG CGTA	694
20	(2) INFORMATION FOR SEQ ID NO:742:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 691 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
	(b) Toronosi, Thear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1482UP	
35	(W) CHESTASSOF	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:742:	
	CATCECCCC TICCOCCCCC TGCCCCAAA GCTGAACCCC TCCCCCCCAA AGGATGCCCAT	60
45	GIGGOGGCIG COCAATTACT CGATGAAGIG CAATGAGGC AACGATGIGT ATCIGCIGCT	120
	CAACOCOCIOC ACCCACOTAC CCTGOCACCT CACCCACACA CTTCTCCATT GGTTGOCCAC	180
50	CACCCAGGAT GAGCCGGTGA TOGAGCTGGT GCTGCGAGAG TGGCTGGAGC TGAACCCGGC	240
	OCTOGRAPHIC COCCULATING TRACEROGRAPS GERRELICCIE COCCUCACO ROCCOCCACCT	300
55	GAACTACTAT GACTACCTGA AGOCGCTGGA GGAGAAGCTG AGGACGGCCA TTGAAGACTT	360

	CONCLACAL GIGALOUISE ARCOSTICCE COALCACACE TITGITECSS ALGIGIALAT	420
5	CCCCCCCCCC TTCACAAAGC TCTCCCTGAT CCACGTGAAC CCCTTTCCCC CCCACACGCCA	480
	CCCGCTGCTG TTTTCATGGA ACGAGCTGTG CACCTGAAGC CCAAGGCGGA AGGGCACCGG	540
10	ACCTROCCCT CGTTGCCGCAA AACTACATCG GTCCCTTCCC GGAAAACAAC ATCGGTCCCT	600
	TOGCAGOGAA AGGAGCACTO GGAACACCAG GTACCTICTIGG ACGTIGGTOGA GGCAGGGCTC	660
15	AATCCGCAAA GCATGCAGAA GCTGGFTGAG A	691
	(2) INFORMATION FOR SEQ ID NO:743:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 581 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
-	(A) ORCANISM: PAG1483RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:743:	
	GATCCAAAAA ACCICTWAAG GIACAGICTC TAATTOCTIC CATSICTTIT TGAACATACA	60
40	TOGACCATOC ATCCTOGITC TIGHTACOGA CAGAATCCTG YAATGCAGCA ATGCCACTTG	120
	GCTOGTTGAC GTGCTTATAA CCACCATCCC TCCAATGGTA TICGCCGGCT TCAGGCAAGT	180
45	TGACACATCT CITAATCKTA AACCTOGATG GATAMCOGCG CTCGTGCAAT GAAAAGGCGT	240
	CTTGSGCAAT GTATTCAAAG GTAACACCCT TAATTCTAGA ACCGGTTCCG GCAAAACACA	300
50	AATCAATCAC TGAGTTATCA ATACCTAAAG CITCAAATAT CTGCGCTCCC TTGTAAGATG	360
	CCAGAGTAGA GATACCCATC TTCGACATGA CTITTAGTAT ACCGCCGTCA ATTGCTTCCT	420
55		

	IGIAAITAIG CAACAGITGC TCATCIGTAA TATCAGAGTA GICATCGTTA ACATTCCGAA	480
5	CTAAACCITC GITATTCATT CTGACCAGGG TTTCCATCGC TAAGTAAGGG AAAATACCGT	540
	CACACCCATA OCCAACAAGA ACACAGAACT GGTGAACTTC G	581
10	(2) INFORMATION FOR SEQ ID NO:744:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 668 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1483UP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:744:	
	CATCATCAGO COCCOCTOCTO COCCOCAGTA ACCOCTOCAC GTOGTAGTOT COCCOTOCCTG	60
35	CTAGTCCGTG GCTCATCGAG AGGTCCTCTT CCTCAGGCTC GGAGTTGGCC AGGCAGGCAC	120
	TICAAAGACT CIGICTICGA TICAATCCCC CCCCCCGIA TICCICCCCC TCGICGCCGIG	180
40	CUTTOGICAG COCCICCOCC TOCAGATOTT CAACGICATO CITCAGCICO TOCAAGITIGG	240
	CAAGAATTOC GGITTOCTIGA GAGACATAGA ATTTIGICAAT TOGOCTOAGC TOCTTATOCA	300
45	GCGCCGCAAT GAATCTTTCG ATGIAGCTCT GTGCAAGCGG CACCCCCTCG GGGTCCTGTG	360
	CARACGICIC ATOCTOGIAC AGCITGICIT TCTGCAGIGI GIACACGAGC TICTTCAACT	420
50	GCCAGTACGC GATATACTTC GACGAACACT CAGGGACCGC GITGAATTGC AGCGAATGTG	480
	AGAACTICAT CITIGGCTTCT ATCGCCTAAC GCCCCTGGTC CGTCCCGATA CAGGTCTGTC	540
55	TCATTGAAAG TACGCAGOGC AGGCATAGGT TTAATTCCAG GCTCCCAGGA GATTTTCGTG	600

	CAAGAGGACG TITTIAATICT CATTATATCA CGTGCCCTGG CTATATTTAT AAAGTTGCCT	660
5	CTPACCOC	668
	(2) INFORMATION FOR SEQ ID NO:745:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 707 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1484RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:745;	
	GATOCTOTTC TATAACTCAA TTAACAATGT TICCTOCTGT GGAGTOGTTC CTGCATCTTC	60
30		
	OSTAACOCTT TCATTCTGAG GIGIAGOCAT TTTTATCTTC TGCGCTGGAA CACTCGGGAA	120
<i>3</i> 5	TICAAATIGA GITATIGGCA CCIGIGCCIC CITCTCCTIG TCCGGTATAC TITCTICAGG	180
	ASSATAAAGA GOCTCOGATG GTGATGATAG CAGTGTTTTC TTAATATOCG GFTCTGAGAC	240
	CTOCGOCTICA AAGOCAGTTA CTGATTOCGA CTGGCGATTC TCCATCGGCG AACTTTGTGT	300
40		
	GGTATGTAGG ATTGCTGGAG TGAGTTCTOC AGGGTTGGAA GAGCTCCTGG CATAGCTAGG	360
45	ATATOTIGGC TCAGGTIGGG TCTTCTCGTA CGGAACAGTG TTGGCTGGAG AGGACTCTGG	420
	TIGICOGIOC ATTIGATAAG TGTATOGAIC AGAAOGTAAG TGTOOCATOG AATATTGTTG	480
50	CGAAAGATTA ATTATTCCTCA ATTGTCTCTC TAACATGGTG TCATAAATGC TCATTATATC	540
	CGAAATTITG GCAITCATGT CTACCAAGGT ATTATATTIG TGAAACGTAT CGTTAAGGGA	600
55	ATGGTTTAAC OGAGGCCCAG TICCAAGGAC CITICTGGTAT AGCATCTGCA GCTGTGTATC	660

	CICTAACACG GCATTICATTG GCTGACCCTT CCTCTTCCTC CACTAGG	707
5	(2) INFORMATION FOR SEQ ID NO:746;	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genemic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1484UP	
20		
<i>2</i> 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:746:	
	GATCTCGGAG AACGTGCTAC AACACTCGTG CCGCGTCAAG CCCGACCCGA	60
30	CCASCASCOS GAGATGAACO COCASCACAC GCCCACTGCG ATOSTGAACT TTGCCTTCGA	120
	GCTGGCGCAG AAGACGCGGG TGACGAACGG GATCTTTTTC CACGCGGTGC GGFTGTACGA	180
35	COGHIACTICC TOCAACCOCG TEGTICCTIACG GCACCAGOCG AAGCTGGTGA TITGOGACCTIG	240
	CCTGTGGCTG GCGGCGAAAA CCTGGGGGGG GTGCAACCAC ATCATCAACA ACGTGACGGT	300
40	ACCUPACION OCCUPACION ACCOCCOCA COCCATOCOCO GIOROSCO	360
	OCTOGROCAC TACTOCOGOG OGTOGRACOT GITTICACCAG TOGRIGITICA COCAGATOGA	420
45	GCGCCACATC CTGGACACGC TGAGCTGGGA CGTGTACGAG CCGATGGTGA ACGACTACGT	480
	OCTCAACGTG GACGAGAACT GTTTGATACA GTACGAGCTA TACAAAAGGC AGCTGCAGCA	540
50	CAATCOOCAG TACOCCAACA AGCGCAACTC GCAGGACAGC AACGCGACGG AGCAGGACGT	600
	GROCCAGGAG GACCAGGACA TOGATAACAA GATOCAGTTA ATCAACATCA AGAAGTTICT	660
55	CATAGACCTG GOOGTICTOGC AGTACGACCT CITGAAGTAT GAGGTATTCC GAGCTA	716

	(2) INFORMATION FOR SEQ ID NO:747:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 748 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1485RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:747:	
25	GATOCOCOCO TTATTIAGCAC OGTOCOTTAA CCAACTOGOC CAAGGAACCA ATTACACTTA	60
	AGAIGCIAIT IGCAGAIATT IGIAGIOCAC ICAAGICAAC ACGCCCATAT ITTACITICI	120
30	AATTOTTAAA TTOTTAACTO TAAGCAATO TAAGTAGTIT ATOOTATOAT CACTIGATOO	180
	TTGCGTTTGT TTGGTCTATA ACCTTEAATT GOGTAGTGCT TATGGAAATA TATATAATGA	240
35	CATATTACAT GOGTOCCATA TAACTTOCGT ATGACACTTT GOCCGAGTOG TYTAAGOCGT	300
	CAGAITTAGG TEATICICCT AAAATCICTG ATATCTACOG AFTCGCOGGT TCCAATCCCG	360
40	TACCICTCAT TATTITITGT ATATTGTCTT TCTCAGGCAT GTGACATTTT GCATCATAAT	420
	CATACCGAAG ATATGGCTCC CACCGTGACC TGATACATTC TGGCATCTGA AGGCATGCAA	480
45	TITTAATOCAA CTGTGOCTOC AGATGCTCTA GGTAGGAACT AGCACAACAT CTAACAACTA	540
	CCCTCCCATA TACACCOCAA TGACACOGIC TGAGTOGTTG TGGCACOCAT CATAAGCCAA	600
50	TICTGATIGE CIGAAGACAG OCTATGAGIC TOCCACAGIC CICCITOCIG TOCCATAGGC	660
	ATATAAATAC CCTTAAAACT CAATTAGCCG GTATTTTATT TGAGCIGCAG AAGGTATCIT	720
55	AACTCAGGIA TAATATACIG TAATGGGG	748

	(2) INFORMATION FOR SEQ ID NO:748:	
5	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 755 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1485UP	
20		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:748:	
	CATCOGAGGT ACTOTTTICG GTGGGCACGG AGCTGTAGCA CGCGGGGTCC AAGAGCGGCA	60
25	THE RECTURE TATESTICS AT CACCICGA TEACCTOCTT GCGCAGGIGC TCCACGTAAT	120
	CITOGGIGGG GAGCCCACAT TOCTICGGGT CGCGGAAAAT GGITGCCAAG TACTCGAGCT	
30	TOTAL CONTRACT CONTRACT CONTRACTOR	180
	CCTCCCACAC CTTCTTGTAT TCTAGCTCCC CGTTCAACCA CACCATGGCC TTGCCCTGAA	240
35	GCATOGICAC CICGICGAGO ACGICAACGA GGICGICGAA TIGIGGCACO GCGCICAGOG	300
35	COCCOTOGAT COCCTTAACA AAGGCOCCCC GOCCCTTCAG GCCCTGTCCA CTAAAGAGAT	360
	CACTOCOCTC GAAAATGCTG ATTGCCTCCC GCATGTACGG CACAAGCTGG COCCACACGA	420
40		120
	ACAGATAGOT CATGTGCCGG GAGTTCGACG TCACGCTAAC TGCCGAGTGC TTGGTTGAGT	480
45	COCTIGAACOG CCTACTGCCC CGGTAGGGGG ACCCGAGAAA TGCGTCATCA CCTCGTCTTC	540
	ATCTGGCTTG AGATACAAAT CCGAAAGCGG CACGTTGCCT GTCATCGCAG AGTTGTTTGA	600
50	CAAGAGCAGC TOGTCTAGTC GCTGCTGGAG CTGGCCCACT TTGCTTTTGA GTAGTTCCAC	660
30	TICACIGOCC TITITOGGATA GCATGAGCIG CAAGIGGCAG TICIOGITIT GCAACGCCAG	720
	The state of the s	720

CACCICATOS GOCOCOSTAC COCTOCTCTT GCAGA

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	(2) INFORMATION FOR SEQ ID NO:749:	
5 10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 729 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1486RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:749:	
25	CATOCITCTT GIACATTTCT CATTITAACA ATGICITCAT AGOGIATATT TIACOGGIAT	60
	CITICTICIG CACCAGACGG ACCTCACCGA ATGCACCCTT TOCTATCACT TTAACAGTGT	120
30	GCAAATCITIC CACGGATAGC CGIGTCCTAC GCAAGCGCAG AAACTGCGAC TCCTTTTTAC	180
	CCAGTGAAGA AAGCTGTCTG TTCTTTCTCT CTTCAGACCA GOCATGAGAT AATAGCTGGG	240
35	ATTCAAGTTC CACGOGTCTT TOGTTGCGCT CAATGGCATG ATTGACAGAT GATTGGTAGA	300
	AATTCTOGAC TTTCAGCTTC ACTGCAGCCG CTTTTTCTTG TGTGCATTTG CTCAGTAGCT	360
40	CTOGACGICT CTCGAAGTAC ATATAGTTCC CCACTCCCGA GGTTTGCCGT TGGCCCCCAT	420
	TGGGCGATTG TGGAACTGAA GAGCACTGCA GGGACTGAGG GGATAGCATA GOGCCCTGCG	480
45	ACCICIOGIT TOCCACIACO GICIGATOCO CAAGOCITOC GICTAGIAGI CCAGGIAGAG	540
	CTGCAGGCTG TAAAGGGGAC TCCGACCCCC CAAACTGTTT ATACGCAGAG GAAGCAGGCT	600
5 0	OCTOCOCACT GTAGTOCCAG CIGITOGAGT AGIGTOCTOG TGAAGAATOG CCGGGGGCAA	660

720

729

CACTACTOIC CTICACCITC CCTAAAACAG TIGITGTICT GOCTGTAAAT CCTOGTCOCC

55

GTAGGCGGG

	(2) INFORMATION FOR SEQ ID NO:750:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 719 base pairs (B) TYPE: nucleic acid	
10	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1486UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:750:	
25	CATCAAAACA GCATGTCTAA GTCTGTTGCC CGCTGCCCCCC AGTGCCCACAC GCAACTGCGT	60
	AAGIGOCTICA TACAGCAGAA CTACAGCATC GTGATTTIGCC CGAACGAGCA GTGCATGTAT	120
30	CCCTTCAATC ACCCCCACCT CATCCACCAC CTCCTCCACA CAACTCACAA CCAAATCCTC	180
	GAGOCTOCAA AGGTGCOOCT GAAAAACGAT AATATCACAG GCAGCOGAGG CGCGCTCATG	240
35	GAATAAGGAA CCAACCGTGT GCTATATACG TGTACTGTCT ATGTTAAGTA GGTCTCGTGC	300
	GCCGCGAGCC CTGCGTGGCT AAAGCTTTAG ATTGGAGTTG TACATGATGT CGCCATCGAC	360
40	CCIGATGCIG ACACIGAACT CAAGGICTIC GICGGIGGAT AIGICCCACG TITTATATAT	420
	CATCATCAAC GOGAACACAT TGCAAATGCT GOOGATGAAC AACCOGTOGA GGTAGTGCTT	480
45	GACGCCCTOG CAGATCTOGT ACGAGATOGT ATACATCAAC ACCTGCCCAG TAGITATAAA	540
	AATCACACCC AAAATGGTCG ACCCTGTCAT CCAGAAGTTG GAGAGCACGA AGATGGAGAC	600
50	CACGAGCTGG CACACCGAGT ACATTAGGAA COOGAGGCCA TIGAGGCCGT ACATTACAAC	660
	GAAAAGGCGG TCGIGITIGI TITCATGTCG GCGIGGTGCT GAATCCAATT TGGTGAAGG	719
55	(2) INFORMATION FOR SEQ ID NO:751:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIH: 703 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1487RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:751:	
20	CATCCACCCC CACCCCATCA ACAACCACCA CITTCCCTAC CACCACCACC TCATACGAAA	6
25	CCCCCACCAC CACATACCCA ACATOCACCC TECTIATCCTT CAACTCAACC ACCTCTTCCA	12
	AGACTIGGGG TCCATCGTGC AGCAGCAGAG CGAGCTGGTA GACCACATAG AAAACAACAT	18
30	ATACACTOCO GTAACCACCA CCAACCATOC ATCTAACCAA CTGTCOCCCC CACTGACATA	24
	CCASCOSCET TOTALCAGET GETSOCIATA TOTGCTTCTC GCTCTGCTGG CATTGCTCTT	30
35	CCTGATCGGG GTGACAGTGC TTTAGAACAT CTCAACTAGT CTACTATGTA ACGCTTTAAT	36
	ATACIACIGE CIGACCIACT CCICCOSCAE TICCCACACE TICACSCASC CEICATOSCE	42
40	GCCGGTCACC AAAAGAACGC GCCCGTCTAA CGCCAGCCAT TTCACCACAT TGATCTCGTA	48
	GACCGIGIOC GOGCAAICIA GOOGGCIAC CACTICCCAC GGGCCAGCCI GIACCICITI	54
45	GIATACOSCO AACACACCAT COGAGOCAAC GCTCGCGATA AGCCCGTCCG CGCTCCAACT	60
	TACOCTIGITAC ACAGCCOGOG TATOCACOGIC COGCAGCACC GTCTCTTTOCA TCCACTCTTT GTCGAACACG TOGGCGTCGT CAGTCAGOCA COGCCAGATG OGC	66
50	(2) INFORMATION FOR SEQ ID NO:752:	70
	And the contract of the stone and the state of the state	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 612 base pairs	

(B) TYPE: nucleic acid

	(C) SIRANDHINESS: single	
5	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1487UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:752:	
	(AT SECONDE DESCRIPTION: SEQ 10 NO: 752:	
	GATCCCAATA CTGGGACTTT ACTAATACCA GCCATGGGGG CAGCTCTGCA GCAGCTGGTA	60
20	The state of the s	60
	ATGACAAGGA GGACAAGAAG AACAAATACT GGAACGCAGA CGCCGAGTAT CTGATCGAAG	120
		120
	AGGIGAAGAA AAACAAAAAG AGIGIAGIAA ACTACCITIGA ATCGAAGACG AAGGAGGAAA	180
25		
	TGACCCGCAA GOGTCTGATC COGAACCTGC AACGATTTIGC AAAGACAATT CTAATGAAGG	240
30	AAGGITTOGA AAACCITOGAG GATATOGICA COCTITICICA TITIOGAAAAT AGACTOCTIGG	300
-	TAGCCCTAAA ACTTAACGAG ACAAATGAAT TTACCAAATT ATTGAAAGTC TATTGCATCA	2.54
	THE THE TATE OF TH	360
	GCCTAGCAGA AATGOOCTIC AAAAATAGAT TGGATGATGT GCTGAGCTGG CTGTATAACG	420
35		120
	ATGGAGAATA CAAGGTTGOC ACAATAGCTA ACGAGAAGCG GGAGGAACTG CTGAAGCAGA	480
40	TATTOGTTOC ATGTOCTICAT ATCCCOCAGG TCCAAAGAGT GACAACCAGT TACCCATCTG	540
	CICTIGGICI TCTIGAIGIA TCTITATAAT TATTGCTAGI CTATAGACAA AGITGGGAAT	600
	CTGAATATAA CT	
45		612
	(2) INFORMATION FOR SEQ ID NO:753:	
50	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGIH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

	(vi) ORIGINAL SOURCE:	
5	(A) ORGANISM: PAG1488RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:753:	
	CARCAL CALL POLITICATE ARTERIA CALCALLA	60
	GATCAACAAA TGATTTTCCT ATTTTCCGCG CACCGATCAA CGAGATATCA TAGGAATCAA	60
15	TGTTGCAGGC AAATCCCTCA CCGAGTATGA AGCTCTGGTA TGCTGTTGGC GTTGTTCCTT	120
	TCATTAACIG COGGICCCTG GGCAGITCCC TTAAGITTGG ATGATCGAGA TATCCACAAT	180
20		
	TIGOCTCATT CATCGICTCC AATCCAATGA TOCAGITTIC TICGAACAAC TCAGGCGCGT	240
	TGTCCTGAAT GTACTTGTAG AACGTCATTA CGGCTTTCAA GAAGTGCCCCC TGGAGGTAGT	300
25	CITGAATAIT TCTACCATTA ATIACACATT TAGGGGCAAA TAACTTGCCG CTAAAAAAGA	360
	CHOMAINT TOTALCATTA MITALACTI TAGGGCAAN TAACTIGECG CINAAAAAA	300
	GAGTGAACAT AGTICTIGGCAG OCTAGGCCGGT AATAGTTTGT GGACCAAATC ATTTCTGGAT	420
30		
	ACTIGICCTIT TICCOCCIGC GICTCIGAAT CGATATAGTA GITGIGCAAT ATGGCAGCCT	480
35	CAGTAGCTIAG GAACCTCTTC GGCTGAAAGC CTGCGCAATG CAACGTCCAT AATGGCGCTC	540
	CITEATCCCCC AGAAAACCGA GACCACACGT CCTGGTGGGG GTCTAGGTAT ACGTACATGC	600
	CIGNOCCC PERSON GEORGE CONTROL OF THE TANK INC.	000
	OCCOGCOTO CTICATOTIT TIAAGCACCA TCACOGIGIA CITCATGIAT TCCTCATOGI	660
40		
	ATATOCOTOG GOOGOCATOC TOCAAGGOOT COCAGGTGAA CAAATAACGG ATACA	715
45	(2) INFORMATION FOR SEQ ID NO:754:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 684 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEUNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(A) ORGANISM: PAG1488UP

(MI) SEQUENCE DESCRIPTION: SEQ ID NO:754:	
GATCTCGTTT AAGCTGCTGG TGAAGTTTGC GAAGGGGTAT GAGCTTTCAC GACGCGAAAC	60
AAACCAGCTG AAGCGGTCTA TGGGCCATGT CTTCCGGTTG GTGCCCCTTTT CTGCCTTCCT	120
GATTATICCS TTICCAGAGI TGTTCCTCCC CTTCCCCCTT AACCTTTICC CCAACATCCT	180
GCCATCCACA TATGITTICIG GGACGGAGAG ACAACAGAAG AGAGTTAAGC TAGAGGAGGT	240
GCGGCGCAAG ACGTCCAACT TTTTGCAGGA GACACTAGAG GAGTCCTCAT TGATCAATTA	300
TAACTOGGIA GAAGGITCAG AGAAGGOCAA AAAGITTCIG AGCITCITOC AGAAGGIGAA	360
CTCCCCTAAG GATGGCAAGA CCAGTGTTTT TACCCCATGAA GACATTTTGT CCATCTCCAA	420
AATGITCAAG AACGACACTG TOCTAGACAA TCTCTCCAGG CCGCAATTGG TTGCCATGGC	480
GAAGTATATG TECTTGEGGE CITTTGGCAC TGACAACATG CITTAGGTAGC AAATGCGTTA	540
TAAATTGAAG AGCATCGTGG AAGACGATAA GAAGATAGAC TACGAAGGTG TTGAGTCACT	600
GAGTACAGAG GAGCTCTATA GTGCCGCCGC TTGGCGCGGG ATCAAAGCCT TCGGTGTTTC	660
TACCGAAGAT TIGGIGGAAA AAAT	684
(2) INFORMATION FOR SEQ ID NO:755:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 728 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDELNESS: single	

(ii) MOLECULE TYPE: DNA (genamic)

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1489RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:755:	
5	GATCACGCCG GAGCACGTGC AATCATTGAA CGAAAGCCCCG GGGTTGCTTG CTTTGCCCGAT	60
	GCACACTCAC ACCCACACA TTACCCGTCA CACTACATTC CTTGCTTTTC CCTACGTTGT	120
o	TCCGGGCGGT CGTTTTAATG AACTTTACGG CTGGGACTCA TACCTAATGG CTTTGGGTCT	180
	TCTAGACTGT AACAAAGTGG ACATAGCACG TGGGATGGTT GAGCATTTCA TCTTTGAGAT	240
5	AGAGCATTAC GGTAAAATAT TGAACGCCAA TAGGAGCTAC TACCTCTGTC GGTCACAACC	300
	CCCGTTCCTA ACCGACATGG CITTGAAGGT CTTCGAAAAAG TTCGGTGGTG ACCAAAATCC	360
?O	TACCOCTIGTIC GATTTICTTIGA AAACAGCATT CATCOCAGCC ATTIAAGGAAT ACAAGAGTIGT	420
	ATGGATGCCA GAACCOCCCT ACGACAAAAC CACCCCTCTT TCATGTTATC ATCCAGATGG	480
?5	TATCGGTTTC CCACCAGAAA CCCAGCCTGA CCACTTTGAC GCAATTTGCC GGAAATTTGC	540
	GGAAAAGCAC AATGTAAGGA TTCCGGAGTT CAGGTGCATG TAGGATGCCG GGGAAGTACA	600
30	CGASCCCCAA CTACATCAGT TCTTTTTGCA TCATCCTGCT GTACGTCACA GTGCACATCA	660
	CACCICTIAC OSICIAGAGA ACGICIGIOC TIACITAGOG ACGATIGATI IGAATOGITA	720
35	CTATACAA	728
	(2) INFORMATION FOR SEQ ID NO:756:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 698 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1489UP

(3CL)	SEQUENCE	DESCRIPTION:	SEO	ID	NO:756:
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5	GATOGTAACA TIGOCCAATA GOTTGITTAG CTOGTCATOG TITCTGATGG CTAGCTGTAG	60
	ATGICTIGGS ATGATICTGG TCTTCTTGTT GTCTCTGGGC GCGTTACCGG CCAACTCTAG	120
10	CATTICOGOG GCCAAGIATT CTAGCACAGC GGITAGGIAC ACAGGCGCGC CCCACCCCAT	180
	TUTUTUTUGO TAGTIGOCCI TICTGAGCAA TUTGTOGACT CTACCGACAG GGAAAGTCAA	240
15	ACCOCCUTA GOOGATOTOG ACTOCCAAGO CTTGCCCCCA GAACCAGOTT TACCTCCTTT	300
	ACCACACATT ATTIGIGTIG TGTGTGTGTGT GTGTGAACTG CGTGTGCTAT	360
20	GAGAAAACAC TACGCTGAAA CTGCTAAATA ATGCAGACAG GTCCCCCCAC CGCAAAGGAT	420
	CCACGCTATA CITCICTCIA CATATITATA CITGICCITT TGCCITCIAA TCCTCCATCG	480
25	TACGOGICIG ACCOTTOAAC AGACCTTOAC TAGACCCTOG ACCTGTGCGG GCTGGTTTTT	540
	TOSCATCACA TETCCGTCCT CETTTTTTCG COCTGAAAAG GAAAGCCCTT COCTCCCACC	600
30	ACCAGAGOG TACTAGCTCT TTCGCGTTGC TGTCCTATGT GCACGCGAAA TTTCATACTG	660
	TAGAGTGTGC CATCAGCTTC ACAGAGTACA ACCGTAGG	698
35	(2) INFORMATION FOR SEQ ID NO:757:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 727 base pairs	
	(B) TYPE: nucleic acid	

- (b) libe: uncleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: INA (genomic)
- (vi) ORIGINAL SOURCE:
- 50 (A) ORGANISM: PAG1490RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:757:	
5	GATGACCITIC CGATACTATG CGAGCCCTTC ACGACATCCA AACTGAAGTC GITTCGAGGAC	60
	CIGAGCOCA TOCAAACGIA OGGITICOGC GGAGAGGCAC TIGCCAGCAT TICTCACATT	120
10	GOGOGACTIAC ATGTGGTGAC GAAAACGAAA GAGAATCAGT GTGCATGGAA GOCTGTCTAC	180
	GAGAATOOOG TAATOGTOGG GGAGCCGAAG CCGACCGCAG GCAAGGATGG GACGACAATC	240
15	CTOGRACAGE ACCTOTTOTA CAATGROOG TOCAGGOTGC GGGGGGTGCG ATCTCCAAGC	300
	CANCACTUTE CCANANTACT OCATOGOCIC COCANCIACE CANTOCATTC OCATOCOCIC	360
20	GGATTITUGT GTAAGAAGIT TUGUGAAACA CAGTACGOGT TAAATGTAGG TUGGACTTCT	420
	TCAAAATCAG ACAAGATACG GOCTGTATTT GGTGCTCCAG TCGTTGCCAA TTTAGTTGAG	480
25	GTAGATATTT CTGCAGACCC TGAGCACGGT CTTACATCCA GTTGGGGCCA GATTACAACT	540
	CCAGACTITA ACAACAAGAA GICTATACCT GCIGIGITTT TCATTAATAA COGOCFIGIT	600
30	TOCTICTICATO CTICTICAGGOG AGOOCTIATICO CAACTITIATO CAACTITOTIG COGRAAGGITA	660
	ACAAACOGIT TATTTACATG AGTTTACACA TAACACOGGA GAATGITGAT GTTAATGIGC	720
35	ATCCTAC	727
	(2) INFORMATION FOR SEQ ID NO:758:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1490UP

(xi)	SEQUENCE	DESCRIPTION:	SEQ	$\rm ID$	NO:758:
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GATCTCAAAG	ACCCAGTACG	ATCGCGTCAT	COCATACATA	AACCACGGAA	ТСААТСААДА	60
CCTCCCTTAC	GAACAGITIG	GATCTGTACC	GCACAAGGGC	TACTATATIC	CTCCCACAAT	120
ATTICIOGAC	GTTCCTCAGA	GCTCCAGACT	CTCCCGTGAA	GAGATATTCG	cccciciosc	180
CGTAGTTGCG	AAATTCAAGG	ACTACGATGA	AGCTATICGT	TACGCTAATG	ACACTAACTA	240
TGGGCTGGCA	TOTIGOGITT	TCACTGAAAA	CATACGCGIT	GOGCACOGCT	TTGTCCGTGA	300
TGICCAATCT	GCACIGIGI	OGGITAATTC	CTCTAATGAT	GAGGAGGTGG	GAGIGCCTTT	360
TOCCOCCTTC	AAGATGAGCG	GTATOGCAAG	GGACCTCGGG	AAGGCAGGCC	TGCAAACTTA	420
CCTCCAGACT	AAAGCAGTAC	ACCIGAACTT	TGCTTAGATA	GAGCAACTCA	TATATTAGAA	480
TCACTTCATA	CATCAACTAT	ATATCATTAT	GIATATCACT	ATGCCAGAGG	TGIAGIGGAA	540
CCACTATITA	TCACGIGATA	GGCG1.1.0CGC	GGTCATCCCG	CCAGUACCUG	CGTTGCAGAA	600
CGCCGGGGGAC	ACATTCAGCA	GGTGCTATAT	ACAGITIGICG	AGGACAGTAT	GGCALGCAGT	660
ACCATTATAG	CAAGTAAGCC	GIGIGCIGIT	TOCATAAAGC	GTAAGGTCAA	GIGGGACCGG	720
CIGGITOC						728

(2) INFORMATION FOR SEQ ID NO:759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1491RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:759:	
5	GATCATCTOC GAATAGGTCT CGGGCACGAC GGACACAAAAG CGCGCGTCCC AGTCACTIGCC	60
	GITCCTGCTGG GCGGGTGCGA AGAAGGAGAA GATGAACGAC CCCGACTTCG ACTTGTGCTC	120
10	CGACGCCAGC TOCTOGACGA COGTIGTOCAC CTTIGACCTGC ACCAGGGTGC CAGGACACGA	180
	CAGAAAGTOG TOOTTATTOT CAGACAGOTT GITCACAGOT GIAGGOTGGI AGTOCACCAG	240
15	COCCHCCCC GCCGCCTIGG CCCCGTCTGC TCCACCACGG ATGTGCTCTG TGTACACGAC	300
	CETCECCTCC ATGTCCACCA TCCACCCCAC CCCCACTCCC CCCCCCAACC TCCTCCACTC	360
20	CASCGATACG AACCGCGGCA GAGACTGCGA GATCGATGAC GCCGCCAGCT ACGCCAGCTC	420
	AAATGICTOC COCATCAGGI AACCOCCCAA GATCATGIAC GAGIGICOGI TCCCGIATIG	480
25	COOCTOCATE AACATOGTOS ACTICAGETT CETETOCTOC ATOCACACOA COCCOCCOC	540
22	ACCEPTAGE COCCOCCATAGE COCCOCCACAAC COCTOCCATCA TOCCCCACAC	600
30	CTCCCCCCTA CCCCCCTTCG TCTCTACACT CTCCCTCTCC CCCTGTACCT TCTTCCCCCT	660
35	CITCICCCTC TCCCCCCCC CCAACTCCAC CCACTCCTCC TCCITCTCCC GTACCA	716
	(2) INFORMATION FOR SEQ ID NO:760:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 729 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1491UP	

(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:760:

	GATCTIGNAL ANAMAGIAGI TIGITATICI CCAGCIGCGC AGICICITCC AGGGITTIAC	60
5	TICCGATECT TATTAATACT GETTCTTTAG ATGETTCCTG ACTITGCCTA TAGCCCATTG	120
	GTTCCCCCCA CTTGTGAAGG TATGCATTGA GAGTCCTCTG GGTAGAACGT GTGGTCCTCC	180
10	CIGIAGITIT AGCAGOGGC TIGGCOGGGA CIGGIACATC AGGCTGAGGT AAAATCICGG	240
	CTGGCGFTGC AGGTTCTATT TCTGTGGGGTG GCTCTACACT AGCATCCAAT ACTTGGGCGC	300
15	TACTACTATC GCATTOGICA ATATCATCTA TGGCCACCAT CACAGAACTT TCTTCTTCCA	360
	TAGOCTOOGA GCATGCAGTA ATCTCGGAAC ATGTGGTAGT ATTATGTAGG TGATCGTCTT	420
20	CGAATGTCCC AATCAGCTCC TGGCTGGGAA CGAGTTTGCG CCTTTTGACC TTCAACTCGG	480
	ASTOTICATIG TOGGACTOSC ASTGACOGTA AAGATTTAGG CAGCATGAGC TOCTGITTOGT	540
25	TAAAATOOCC GICCAGITIC TCIGCTAAAC TTIGCAGGAC ATACICITCA TIGIGAAGCA	600
	ATACAGICCT CITATOCOGA GICACATICA CGICTACAAA CTOCOGOGGAG AGCICAAAAT	660
30	TTAGAATAAT GACGGGATAC TGGACGTTGT TGAAGCTTCG ATATATGTCA TTGCAACACT	720
	TCAGGACTT	729
35	(2) INFORMATION FOR SEQ ID NO:761:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGIH: 610 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1492RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:761:

	CATCHACTIC TOCAACAACG ACCITCUIGIG GICCAANTGOC TACCOOGIGA ACCGCTITIGG	60
5	CCAGGGGGG TICCGCATGC TIATCGAGGG CCTGTACGGC GAGCTCAACG CCGCCTACAG	120
	CCTGOCCCAT ACCACCTACG GCAAGCCCAA CCGCATTGCC TACGACTATG CTGCCCGCGT	180
10	CCTGGGCGCC TGGTCCGGGCC TCCAGACCGCC ACAGCCGCCC GCCACGGTAT ACATGGTTGG	240
	CGACAACCCC CACAGCGACA TAATAGGCGC ATACAACTAC GGCTGCCGCA GCTGCTTGGT	300
15	COGTAGOGGO GTOTATOGGO ATGGAGACAC GTTACOATGC CAACOGACOO TOGTOGTOGA	360
	CTCCGTCFTG GACGCCGTAA CCGCCGCTCT CCAGCACTCT TCACATTAAC TTCTATACTT	420
20	TTACGICTIC TATATACCCG GCTCGTCCGT CCGCAGATGC CTAGATCTGA ATCTTCGCCA	480
	CCACAGITTG CTCCTGAGCC AACTIGTCTG CGFTGCGCCG GCGCATATGC TCCTTGCACG	540
25	TOOOGAGOOC GOOGGAGGTA TOGTTTTOCA TOAGCOOGTIG GOOGGAACAG AACTGGCOGT	600
	CACAGAACTG	610
30	(2) INFORMATION FOR SEQ ID NO:762:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 553 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1492UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:762:	
50	CATCATGITG GIGGOCTOCT GOGIOGOCTG CGGCGTGAAG TIGGGGTTTG ATTCCGCCAC	60
55	CACCOCTEC CICACCOCT TCATCICCC CACCITICCC TCCACCCCC ACCCITICIA	120

	CTCGTCGGCC GACACGTCGT CGTCTAGGGA GAGCTGCTTC GAATTGGAGT TATTACTGGAG	180
5	CATTOSTIGAT CTOCCTIGTOC GCAAGAGTOG TOGAAGACGT GITICTTTGGC CTGTTCGCTG	240
	AACAAAGCAC TOOGTGTTTT TOATGGAGGG CGTGGTCCCCA GGAGCGCAGA CCGGAGAAGC	300
10	GASCGICAGE GCCGCGCGC AGGGACGIAG GCGGCTGCTC CCCACTATGT AATGCTGGAT	360
	ATGAAGAACA GAAATACTAG ATAATATATT TGTATTAGAC AGTCGTGCGG ACCGGCAGAG	420
15	OCCOCCUTTO ACAAGTICCOC ATOSTOCTCA TOCCOCAACG CCAATGCCGT AGCGCGCTCC	480
	AGCTCCTGCT GGTACTGCTG CATCAACTGC TGGTCCCCCT GCACCTCTGG AGGCGCCTAG	540
20	GCAGGGGAGC CAC	553
	(2) INFORMATION FOR SEQ ID NO:763:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1493RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:763:	
45	GATOGAATAA AGTAGGITIG GOGCTGACOG GCATCACOCG CGCACGTAGC GGGAACAAGT	60
	TOCCOGRETA AATEFTTOCG TAGTOGATGA AGGIATIAGT ATTCATCTIC TOCAGCAAAG	120
50	ACAATTCATA CTGTTGGGGG GGCCGCGAAG AGTTACCAGT GTATTCTGCC AACGCTGCGA	180
	COCTICOGCA ACTAGATITCS AGRICOCTICT GGAGCTCTGA AACATTATCT AGGATGTTGA	240
5 5	ACOGATOGAA ACCOGTIGTOG COGGGCATAG COGACATOGC AGTTCTCAGA TTCTGCATAG	300

	AACCOCCATA TAGAGCCAGT GCCTCCTGAT GCTTGCCTTC CTCTTGGTAA AGGGGAGCGA	360
5	GCCCCCCCCC TACAAGCTCC GCACGGTAAA ACACCTTGAC AAGCTTCAGA TATGCAGTGA	420
	OCTUATORIC TGAGTAGACA COGOGTAGAC COATAGOCTIC CTOTOCATOG GTGATTATGT	480
10	TOTICATICAC GIGGITICAGO TOCTIGIACT TOGICAAGOG AGCOGIOCIG COGCOTICIT	540
	OCCATTOGAC CCACAGAGGT TOCAACAGGG CAACATOGGG GCCCATOGTC GCGCACAAGT	600
15	AGTIGAATIG GAGGIAIGIG AGCAATATOT GGTOGTOCTO TOCCTCATAG TGCACACCTT	660
	CCTCCTGTCT COCCTCCATT GACTGCCTCT GGGCATCAAT TGCCGGGTTC CACTTCAGT	719
20	(2) INFORMATION FOR SEQ ID NO:764:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 726 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1493UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:764:	
	CATCATACTT ATCCACCOGT CAAGCCAGGT CTCAATCTTG ACGATGAGCC AGCCCGCCCG	60
45	OGTOGOCATO TOGAGOCAGO GOTOCOGGAA GOCAATTAGG TAGOCTAGAC CAAGOCOGAT	120
	TAGGTGGCCG ACAAAGCTGG AGCCGGGCAT TAGCAGCGTG ACAAGTACCA GGAACACCAG	180
50	COGGATATAT AGGGTCGGCA TCTTCAGACT TGGGAGCTCG TAGTGGGGGC GGAAGCCCGC	240
	CTOCTOCACT GCGAAGTAGC CACACAGCGT AAAGCACCAC CCGCTGCCCC CGCCTACGTA	300
55	AACGTTTGGG TACAACAACA TGCCAACTAA GCAGTACACG ACGCCGGTCA CAATGGCCAG	360

	CACCITICACC GICATICCCG TAAACACCGI CCCGIGICAC GCTTOCAACA TCCACACCGG	420
5	CACAAACAGC GACATCAGAT TCAACAGCAA ATGGAACATT GACAGGIGGG CCAGIGGATA	480
	GAGGGAGAGC COGGTCAGCT GCAGCTTCCT AAGCCCCCC GGATCCAACA GGATCTTCTC	540
10	GITGATTOOG AACACCCAAT TCAGCACATA CACAAGCGTA AGGGAACACC GACAAGCCTG	600
	CACTAACACC GCCCGGCTTA TOGACCCCGG TCCGTAACAT CGACTTCCAA TCCATCTTGC	660
15	TCAATCAAAG TGGCAGITTG CTTGGGCGIG GCAGTGGACT ATGCCTCGCC AGTTGCCCAT	720
	CAAAAC	726
20	(2) INFORMATION FOR SEQ ID NO:765:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
25	(B) TYPE: mucleic acid	
20		
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1494RD	
35	(A) ORGANISM: PAG1494RP	
<i>35</i> <i>40</i>	(A) ORGANISM: PAG1494RP (XI) SEQUENCE DESCRIPTION: SEQ ID NO:765:	
		60
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765:	60 120
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765: GATCTICGIT CGIGAAAACC TIGCACGICT TCAIGAGCIC AAGAATIGCC TCTGCATCIA	
40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:765: GATCTICGIT CGIGAAAACC TICCACGICT TCATGAGCIC AAGAATIGCC TCTGCATCTA TICTGICCOG TIGGATICIG CCTTCCTTAT AGICCTGAAT CATGGGGCCA AAACCCCGGG	120
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:765: GATCTICGIT CGIGAAAACC TIGCACGICT TCAIGAGCIC AAGAATIGCC TCTGCATCIA TICTGICCOG TIGGATICIG CCTTCCTTAT AGICCTGAAT CAIGCGCCCA AAAGCCCCCG GCGICCAGIC ATGACGGGAT CGGCCCTTAT AGGACTICCC TGCAAGCCCC ATGACGCTCC	120 180

	CCACIOCITI AITIGICAAG CAGAGGATTA GIATITICATT AGGAGCIACA AICOCTIOGI	420
5	AAACCAGGIT GI'AGACTTIA TOCAGIAGIG TCACOGICIT GCCAGACOCA GGICCCOCTA	480
	CCACATTGAC AGTIGTACAA GOCTCATAIG GATGTGTTAC TACTOGTGAT TGGGACGTOG	540
10	TCAGTOCTIT CATTCATGTA TGATACATOC TCGAGCGTCG GCGAAGGAAA TAAATTCGTG	600
	ANTITICCGTT TTANGATACT CAAAAGAGAT GAGATAACOG COCOCAAGOC OGAGTAGAAT	660
15	TACAGCAGCT ATTGAATATA TITAGTITAT TTATCTOOCT AGCTTAACCA CTAGTGT	717
	(2) INFORMATION FOR SEQ ID NO:766:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 606 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genemic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1494UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:766:	
40	GATCCITTAG GCCATCCTCT CCAAATTACC CGTGCTTGGC TTCAGTAGCT CAGTGGGAAG	60
	AGCGICAGIC TCATAATCIG AAGGICGAGA GITGGAACCT CCCCIGGAGC AAGITITITIG	120
45	ASCERCAGIC TCATAATCIG AAGERCGAGA GITICGAACCT CCCCTGGAGC AAGIFFITTIG CICCGGGAAA TAAGTATTIG GAGCTGGACT GAAGGGCCAA CCTATGCAGC TITIGCTGGIG	120 180
45		
45 50	CICCOGGAAA TAAGTATTIG GAGCIOGACT GAAGCGCCAA CCTATGCAGC TITIGCIGGIG	180 240
	CICCESCAAA TAAGTATTIG GAGCIOGACT GAAGCOCCAA CCTATGCAGC TITICCIGGIG CGAAGTGITC ATTCATGTCT GCGGACTATG TCTATATATC TIGCGCGICT TGTTCTTCTG	180

	GIASCARLO ASIASOARIG COCAGNICIT TOGOCTTATT GIAACAGAGA OCTITIGIOGO	480
5	OGTICITETO CACAATOCOG COCACTATAT ACGTOGIACO GGGTTOCAGO GICTOCAGOG	540
	TOTCATCAGI ATCTOCAGIA AGGIAAACTG CGTTCGTAGT TOCAAGGOGG GATTCGTCTG	600
10	TGAAAT	60€
	(2) INFORMATION FOR SEQ ID NO:767:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1495RP	
	THE STATE OF THE S	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:767:	
35	CATCGAATTA GOOGGITTTA ATGAAACATA AGGAACGAGG TCTAAATGOG CAACATCCTT	60
	CAATOCAGIG CCAACATGIA TOCCGITCIT GGTAAACAAA AITGIACCAT OCACATAGIT	120
40	AATGCCACAT CCGATCACGT CGTCTCGACC ATAGGGCTTC GAGTACGACT TGAACAAAGA	180
	OCCURATET ATGRAACOGT COCACCOGTT GEAAATGRAG ACATOCTEAC CAGROCIACT	240
45	CTGTTGCCAA GTTGGCCTCG AACCCTCAAA AGGCCCTCTT AATATGTTGG AAGTTTGCCG	300
	GITCAAGGCA GAAAATTCAC CCGGGICCCT CGAAGGIGGA TCGCTAGIGT TIGCITCGCC	36 0
50	AGCATTIGAC OCCACITTIC ACCACICCTT AAATCCAATA TICATATIOC AGGITTOGCC	420
	TGACTGOGCG CTGGTCACOG ATAGTACCTT AATTTCATAG TAAAAGATAG CCACTTTCTT	480
55	ATCATTAATA CAAGCATTOG CCCAGGIGGA AGCCCACTGC TGCTTCIGGT TAITAACTGA	540

	MSICCOLMSC CIMITALLIA COMINSSOCI GITGICALMS COMENSIACA OCTOCONSTI	600
5	COOSTIAGRO COCAASTITIS TGAAACCOTC TGITGAGACC AAAACTGAGT TGITCGACTG	660
	TOTOGICCAG AGGIGGGCCA AAAGGATACC TATCGAGGAG TATACGTCTG AGAAA	715
10	(2) INFORMATION FOR SEQ ID NO:768:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1495UP	
25	(10)	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:768:	
	GATCAGCCAA CAGCIGAGTT CIGATTOGAT GAGAGCTATT AGTAAACTTT TIGTGTTTAC	60
35	GETGCTGGTC CTGGGATCGT TACAGTACTA CTGTGGACGC TACGGCGGGT GCCCCGGGCA	120
	GATTOCAGTG ATAAGCCATT ATACGTGGCC TTGCACGTAC GCGCCGGCAG TACGGCATAA	180
40	ATTAGGGAAG GOCAGGGAGT GGTAGGGGGC CAATGGGGCT COGCATGTGT CGGTGGGGAG	240
	CCCCTCGACCCAACC TCATCCCCCA CCTCGACCCAAA GTATCCCAGT GCACCCACAA	300
45	GCATGTACAA CCGCGCATGC GGCAGGCTGG CGCGCACGCG ATAGTAACAG CGCGCGTGGC	360
	ATOGAATIGTC GTACAGCAGT ACCAGCGGGG GCATGTGGTG CCTCTGACAG GGGGACTGCT	420
50	GOOGNAGICI COGIGICICG AGAGGIGGGC CGAAGAACT GCGCGCGCCT GGCAGIGGCT	480
	CIGCAAGCAT GCTCGGGGGC TACCACAGCA GTACAGCAGC AGTATCCTGC GTTTGTGGCG	540
55	CATATOGGGG GCATATOGGA GCCTTTGCAC GGCGCCTACA ACCGGATCTA TCTGGACTTG	600

	COCCOCCAR ICCARCARA GACUICCEAG CACSCAGIOC COCCCCCOCG COCACTCAKT	660
5	ACATCACATC CACTATCACA ATGACCATGA CTCOCTOGAT GAACTC	706
	(2) INFORMATION FOR SEQ ID NO:769;	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 749 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYFE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1496RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:769:	
	52 ID NO: 769:	
30	GATCGTTTTC TGTCAAACCG CAGTCGGGTT CAAGCAGTAC GTTGAATTTA GCTCTTGCAT	60
	TCAACAAGIC TITCCCAGIT TCCACAATGT TGTCGATAAT CAAGGGTTTA AAGTCTAGAA	120
35	CCTCTTCTTG CGTGAAGCCG TTCTGGTGAA CAATCTTCAG TTGTTGCAGT ACGGTGGATT	180
	TCCCGCTCTC GCCAGAACCC AACAACAAAA CCTTGAGCGC GCGATTGCTG GCACTGGGTT	240
40	GCCCCATTICA CCCTGGTCCA GCCACTGCCG TTGTCTGCTG ACTCGTCCCG GATACCACGG	300
	ASCULTUCCT OCCUCCOCT GTAGCOCCGC ACGIGCTATG ACTGGGTGAC GTCTCAGGTT	360
45	TEACTICIEC ACCEPANTET ACCEPTITE CICCIGITIC TACCITCICA GAAGCACCAT	420
	GICIGICCIG ACGCCCCTTT TCCCCCGIGIG TICCTGATCC CTIGICCTTC GACGCCACA	480
50	ACCOCATTAT GICGGGCTCT ATTATOCACCA GIACTTOGAG CACTCTAGOG CCTGGCTTTC	540
	TITIGAAATAT TACCGIUCOG GCAAAAGCCA CITATAGCGC CIGATCAATG GATTCCACTG	600
55	CTAGAGGCTA ATTAGGCTGC CGCTTGTCAC TTCGCGGGCC ATCACATTAT ATTCATAGCA	660

	AASTASSIGE CAACASAANA MAICAGEEG CETECTITAT TEATENESIG AACAAATECA	720
5	CATGAACAAT CACGTGAACA CACATTTGG	749
	(2) INFORMATION FOR SEQ ID NO:770:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 754 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1496UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:770:	
30	GATOGAAGIC AATGCCAGAC TATCTCGTTC TTCTGCATTG GCGTCCAAGG CAACAGGATA	60
	CCCCCTTGCC TATACTGCCG CTAAGATTGC TCTTGGGTAT ACATTACCAG AGTTGCCTAA	120
35	TOCTOTTACC AAGTOGACGG TOGOCAACTT TGAACCCTCA CTGGACTACA TTGTGGCCAA	180
	GGTTCCAAGA TGOGATCTCT CCAAATTTCA ACACGTGGAT AAGACTATTG GGTCTGCCAT	240
40	GAAGTCCGTA GGTGAAGTGA TGGCGATCGG CCGGAATTTT GAGGAAGCTT TCCAAAAACCC	300
	TITCCGICAG GITGATCCAT CICTACTAGG TTTCCAGGGC TCTGACGAAT TCGCAGACCT	360
45	AGATGAAGCC TTOCAATTTC CTACAGATAG AAGGTGGTTG GCTGTGGGAG AAGCGCTAAT	420
	GAACAGAGGT TACTICTIGTIGG AACGTGTACA CGAGCTTACG AAAATTGATA GATTTTTCCT	480
50	GCACAAGIGI ATGAATATTG TOOGAATGCA GAAGCAATTA GAGACCCTAG GATCAATAAA	540
	TOGGCTAGAC GAGGTTCTGT TGCGGAAGGC TAAAAAAGCTC GGCTTCTGTG ACAAGCAGAT	600
55	TOCACOCCCT ATTITCAGATG ACCICTCTGA ATTOGATATT ACACCCCTCA GAAAAAGCTT	660

	TESCATITIG CEATTIGITA AACGIATOGA CACCATESSES GEAGAAGITE CIECOGIAAC	720
5	CAACTACTTG TATGITACCT ATAATCCGGT CAAA	754
	(2) INFORMATION FOR SEQ ID NO:771:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 740 base pairs	
	(B) TYPE: nucleic acid	
_	(C) STRANDETNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1497RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:771:	
30	GATCATTTOG TCTTCTTOGC CTCTACAAAC TGTGAATATC ATACTAGACC TGAAGTCAGG	60
	TAGGGAGCAA COCCAACOCTT CGGTCGCAGT AGAGGCTGGC AAATCCATTA AAAAGACCGA	120
35	TICGAATOOG AACTOTAAAA TIGAAACTAA QCAATTICAT GAACTOTOGA CAGTTOOTOG	180
	TCTTTCCAGT ATTGACTATT ATAACCTTAA GAGAACGTAT CGAACTTACA AATCTCTGAA	240
40	AAGGGCCACT ATTGAAGATA TATTACATGT TGTTGTCCAC AGAGATCTGG COGAGCGCAT	300
	TOTTACTOAT ATOCAAAGAG AATOTGAGOT GCAACAATAT GAGGAGGATG GCAGGAATGA	360
45	GETATGAAAT GITCCCCATT TGGATTAAGG TATCAGGTGG TCACGATATC CACTATATGG	420
	TOCTATTAAC GOCATGCAAA GTGTAGAATT AACCTAAAGA ATATGTTATA TATATATATT	480
50	ATAAACTACA AACTAACGGA COCAATGAAA TCTAAGTGTC GCAAGGTTAG CCTTAATACC	540
	GGTACTTGGA TAAAATCTCC TTTTTCAAAT GATACAAGCG TCCCATTTCA AACGCCATGC	600
55	CACAATCACT GOCTGGATTC ATCATGATTG TGATTGCGGT TGCCTCAGTC GGAAATAAAT	660

	TAGCAATACT CATTATACOC TTCGOGACCT CCAGCOGCTT CTCTTGGGTA GGTTCAAATG	720
5	AGGCAATTIG CATACICTIT	740
	(2) INFORMATION FOR SEQ ID NO:772:	
10	(i) SEQUENCE CHARACTERISTICS:	
, ,	(A) LENGIH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1497UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:772:	
30	GATOCTICTICA CAGCOGOCGA COCCOCAGOC COCCTIACOGO GACCTICCAGG ACGAGOTICAA	60
	GETAGRAGUE TOORAGOOR COTTTOORIA TOORGOOTTIG TTOORGOORA TOORGOOG	120
35	COCCCCCCAG GATGOCCAACA ACTTGGTGCC GOOGTGOCOC CCATGGTGAC	180
	GCCGCACCTT CCCATGGAAC CCTCGCAGCC GCACGGGTG CCACAGCAGC	240
40	CCACCAGCCA CAGCAGCOG COCAGAAGOG AATGCACATG CTCCAACAGC TGCACGAAGA	300
	GCAGAAGAAC TATTICTTACG TGGACCGCCA ACCGTCAATT ATGCAACAGC AGCCACACAT	360
45	GATOCAGCAA CTGCCGCAAC AACGGCCTCG GATGCAGCAA CTGCCGTTGC AGGGCCAGTC	420
	CGAGACOCCG AAGCCCGCAG GCAGITICICC AATGGTGGTG CCCGTCAACC ATAGGCAGCT	480
50	GITOCAGAAC CICCACCCCA GCATCCAGAA AAGAGTATCA CAGGATCTGA ACAGCAAGCA	540
	GIATGAACTA TTTGTGAAGT CTTTCATGGA ACATTGTAAG COGTGTAATA TTCCGTTAA	600
58	CCCAACCCTG AGATAGGCGG GACGCGGGTG AACTTATTCA TTTTATACAT GTTGGTACAA	660

	THE THEORY OF THE PROPERTY OF	720
5	(2) INFORMATION FOR SEQ ID NO:773:	
	(2) The Grant Cold For Seg ID NO://3:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 713 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
15		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1498RP	
05		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:773:	
	GATCACTACG TGACATTOGG TACGGAATGG CACTCCAATG COGACAAACC TCTTCCTACC	60
30	CONTROL COMPA	
	COGRECTEA COCOGNICIG COANCIACON CACATORIGO CONTACCOC ACCONTORG	120
	CACCAAATTED ACTICCATIANTS CHIRATIAN CAN	
	CACCAAATGT ACTOGATATC GTTATTACAT GTCTACGCCC TCACGTGCAT CCACCATCTG	180
35	ATATCATGTC TOCTCTAGGC TATATATTTC GGTTGCGGCC ATATCTACCA GAAAGCACCG	
	MINIMITIC GGI IGCGGC ATATCTACCA GAAAQCACCG	240
	TITICCOGTICC GATCAACTGT AGTTAAGCTG GTAAGAGCCT GACCGAGTAG TGTAGTGGGT	
40	CHARLESCE CALCUADIAG IGNACIOGI	300
40	CACCATACGO GAAACTCAGG TGCTGCAATC TTTTTTTTTT CCTCCTCCTG CAAGCTGGCC	260
	Control Control Control	360
	OCCAACACAG GICACCCIAG TATOSCICAC ATOCAATICA CATAICIACI TCIGACIGGI	420
45	The state of the s	420
	CIUGIOGOGG AUGOCCATCA TUGCAAACAG TUTGCTCOCA TOGGACTITA ACGACCTCOC	480
		400
	GATAATAATC AGAGATOGTC TACITTATAAA ACATCAGGCA CAAAAAGAAA GGTGCAGOGA	540
5 0		340
	AATGGTATAT ATAGGTCCTC CAGATCCACC CACCGGTACC TCCTACTTGG CCGTATCTGC	600
	GICTOCOTICE COCTTICCCCC TGAGATCCTG TCCCCCGAA ATGTACTCTC AAATCCCCTT	660
5 5		

	GITCAGTGCC CCATACAGCT CATTAAGCTC AGTGCCCCCG ATGCTTAGTA GTA	713
5	(2) INFORMATION FOR SEQ ID NO:774:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1498UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:774:	
25	CATCTOTTOG TTOTOGCATO CATGAAGAAC OCAGOGAATT OCCATAAGTA TTOTGAATTG	60
20	CAGATTITOG TGAATCATOG AATCITTGAA COCACATTOC GTCCTCTOGT ATTCCACOOG	120
30	CCATCCCTGT TICACCGTCA TTTCCTTCTC AAACCCTCGG GTTTGGTAAT CAGTCATACT	180
35	COGTOGTAAG ACAAGGTTAA CTTGAAAATG CTGGCCATGG GCGCAACTTG CGCGCACTGC	240
	GETCTGAGCT ACTITICIACA CTGCGTATTA GETTTCGACC ACATOGTGCA GTGCACCTGG	300
	COCTICAAGA ACCIIACGACA AACAAGGCCI TOCAGGCGAA TAGTATICCC AAAGIITIGAC	360
40	CTCAAATCAG GTAGGATTAC CCGCTGAACT TAAGCATATC AATAAGCGGA GGAAAAGAAA	420
45	CCAACCGEGA TIGOCITAGI AACGGCGAGI GAAGGGCGAA AAGCTCAAAT TIGAAATCIG	480
45	COCCUTICGG CETCCGAGIT GIAATITGAA GAAAGTACCT TOGTTOCTAG TCCCTGTCTA	540
5 0	TGTTCCTTGG AACAGGACGT CATAGAGGGT GAGAATCCCG TCTGGCCGGG GTGCTAGTGC	600
- J	CATCTAAGGT TCTTTCGAGG AGTCGAGTTG TTTCCGAATG CACCTCTAAG TCCGTCGTAA	660
65	ATTCCATCTA AAGCTAAATA TTGGCGAGAG ACCCATAGC	699

(2) INFORMATION FOR SEQ ID NO:775:

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 742 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1499RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:775:	
25	CATCACCTIC ATCGATTACC CAGAATTCCC CTTCAACACC AACGAGGCCA COGAGATGCC	60
	CITCOGCTAC GTACTGGACG CTGCTGGCAG GCCCATTCTG CCATCAGGCA TGCTAGAGCT	120
	CATCAAAAAG GACTOOGAAC AGAGTCTOGA TGACCTACTT TAGGCTOGTT GAACAACAC	180
30	TTATAGATGA TGTATATATG COCGTCGTCC CCCAGAGACT GGCATCGGAA GCCACGCAAC	240
35	CTAAAGICGA TAGAACICTG TCAACAGAAT CAGTICTTIT CCTCCTTCAG CATCTCGCCA	300
	AGCAGCTGCT CGAAATCGAT ATCATCAGAA GTGGTTTTTG CAGGAGCAGC TAGGGGGGGC	360
40	TECTOCGACE CACGICCTCT AGCCTTGTAC AATGACACAC CCCCGAACAG CGTCAATACC	420
	GTOCCANGCA CCAAAACATG AGGCTGAACC GOCTTTCCAA AGATGTTGTA AGCTTGACCC	480
4 5	ATCOCTAATC ACCGAATCCG CTOCAGATAT GOOGTCTCAT GGTCTGGTGT GTAGCOGTGT	540
	GCATTIGICA GCICCIATIG GCGCAGCAGG CAAGTOGATC TAGAGGGCTA CAATGAGGIG	600
50	TTCGGGTGTT TGTCAGGGTA CGGAGGAGGT AGCACGTCAT CGTTCAAATA TCTGTACCGC	660
	CCCATGAACA TCTATTCGGT GCATTGGGTT TOGAGCACGG GCGATCATTG GAGACTAACA	720

742

55

CTCACGAATT TTGCCTGGCG GA

	(2) INFORMATION FOR SEQ ID NO:776:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 716 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) Original Source: (A) Organism: Pag1499UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:776:	
25	GATCOCAATG GAGAAGGIAA COCTOCTACC GAAGGITATC AGTGTTTTGA ATAAGGCGAA	60
25	CCTIGCAGAC ACAATTITIGG ACAATAATTT GCTACAGAGT GTGCGGATCT GOCTTGAGCC	120
30	ACTROCOGRAT GGATCOCTIAC CATCCTITOGA GATACAGAAG TCTCTCTTTG CCGCGATTGA	180
	GAACCTCCCC ATAAAAACAG AGCACCTCAA GGAGAGCGGA CTGGGGGAAGG TGGTCATATT	240
35	TTACACCAAG TCTAAGCGTG TAGAACACAA GCTGGCCCGG CTAGCTGACC GGCTGGTTGC	300
	AGAATGGACG COCCCIATTA TOOGCOCTIC CCATAACTAC COOGACAAGC GTGTCCTGAA	360
40	CATOCACTIC CACCIOCAGA ACCACCCIAA GAAACCCCCA CITGATTCIG CCAAATCIAA	420
	GARACOGAGA ARGOCTOCAG TOGACGAGGA GARACACAAG TCACTCTACG AGCTTOCCGC	480
45	TGCCAAGCGG AACACAGCGC CAGCGCCTGC GCAGACAACC ACCCATTACA AATACGCACC	540
	ASTICACIONAT ATICTICGANCE TACAGNICOS GATICOSCIACE GCAGGICGIOG GCTICCACIOCT	600
	CAACAACAAC GATCTGTACA AGAGACTCAA CTCGAGACTT GCCAAGTCTA AACGGTCCAA	660

GTAACCGCTG TGTACTTCAG CTAATAGTAT TATAATAACG TTTAATGATA CTGAAA

(2) INFORMATION FOR SEQ ID NO:777:

1037

716

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIH: 719 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1500RP	
15		
2 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:777:	
20	CATCACCTAA TOCCTOCTTG TCAAAGACCA AATCCTTCAC CCCTAGAACT TTTCCTAGAG	
	THE	60
	CATCCATTCC CATAACCIAG GICGCITIGI GICCITAAAG AATATIGGIT TAAITIGCIT	
25	AND THE WINTERS THE	120
	TUGOGGACGG AGTAAAGOGT TATGIAGCAT TITTICAAAAG AGGUITAATG GACACATCCC	100
		180
	ACCATACTAT CAATCACAAA CTCCAATTCC TGCCACCATT CTCCTACTTC TTATATTTAC	240
30		240
	TGITATACAT CTACTOCAGA GTCAAGCATA TATACCAAAT AATTCACCAA ATACTAGCTC	300
		300
	TICHAAGICT TCAGCIGATG GATTCGCCCC AAGGCCCCC AGAGCIGCAG GHAGGIACCC	360
35		300
	ACACCTICCA AAATOCICAT GIGOGIGAAT CCIATTICIT TAAICAICIC CAGOOGCAGG	420
		720
	GETTETTIAA TETETGICAA GITETTEATG ACACGCAAAC ATGTAGTCAT TATGTCCACC	480
40		400
	GCCCAGIACC THIGCCCCAC AATHCGCGTA AGTAATTGAG CGACTCATCA AGAGTAGCAG	540
		340
	ATAGCAGCAT TITICTICATG ACCAGGGGAT GCGGGCAGTC CACTATCTTA AAAACGTTGT	600
15		-
	CCCCCTTCAC TAACCTCAAG CCCCCCACG TCCTCTCCAG ATTGTTCATG CCCTCCCCCA	660
	TGTCACCTTC CCCAGTGAAT ATCAGCCCCT CCAGACCATC ATTGGTGTTC TGTACGTTT	719
50		
	(2) INFORMATION FOR SEQ ID NO:778:	
	(i) SEQUENCE CHARACTERISTICS:	
5 <i>5</i>	(A) LENGTH: 664 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1500UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:778:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 176:	
	GATCOCCACC COCCCCTCA CCCCAAGGCC CCCCAACCCC GAGGAGCACA TCAATGGCTT	60
20	TGACCTCGAG GCGCCGCCCC AAAAGAAGAC CAAAATACTA TAGTAGTACG TACATTGTAA	120
	TACATOCOCA AGACTITOCCO CCASTITAGOC GOCCOCCTOC CAGGITOTICA OCAGOGOCCO	180
25		
	COOSTOOSCA GACGICCICA CCAGCIGGCG CCTACCCICC TIGIAGACGG TGICAATGAC	240
	TECOCCOCCA TOCACACACO CCACCTOCTO GCACACCACT ACCTOCCTGG TCACGTCCAC	300
30	TACGUACOG TACGOOCAA CATAGOGUTT GUCCUCTAGG AAAGOGCACC GUGCCAGGAG	360
	INGIAGOS IAGOCOM CAIAGOSITI GICCICIAG AMBOGAC GIGOCASMS	200
	CONTROCOURS TROCOCOCAG GRACOCCAAA TOOCCCCCTT ACACCCTURIC COCCCTCCTG	420
35		
	OCCUTANANG CICACACTUT CATOGRADOC CAGOGORCAC ACCITOCICIO CATGOGOGGA	480
	ASTOCACAGE GAGGICACAC CACTECOGGIG GOCOGGICTIOC GICTIOCACA CTGOGTOCTC	540
40		
	OCTOCOCCC TOCTOCTACC CTCCTACCAC TOCCTCAATC CCCCCACCTCT ATACCCCCCC	600
	GOOGAGACC GOOCAGACGC COOCTGATAG CAGCGGAAAG TCGGTGGCCA CAAAAGCCGC	660
45	COOG	664
	Case	009
	(2) INFORMATION FOR SEQ ID NO:779:	
50		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 696 base pairs	
	(B) TYPE: nucleic acid	
5 5	(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1501RP	
70		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:779:	
15	GATCTATITA AATATAACAT ATTATTTATT TCTTTTTTTA AACATTTTAA ATTTAATTAA	60
20	TTATTTATTT ATTTAATTAA TTATTTTTAT TAGTTAAGAT AATTTTATAA CTTTAATTAG	120
	AGAGCTAAGG TACACACCCC TAATGCTTTC AGCATTCTTG TGGTACCACT CTAATTAAAG	180
25	AGITATTATA TIAATGATAT AATATGTAGA TATTCAGITT TGAACTGAAG ATATATGTCC	240
	CTAAAACATA TGITTTACCA ATTAAACTAT ATOCACTAAC TITTIATTATA TAATTTAATA	300
30	ATTAAGAATA TITTAAGATT GAATTAGAGG AGTATTAAAT GAATGAATAA GAGGTOGTGA	360
	ATTTAATATA AACTCAATAG ATGATGATTT AGTAGTATTC ATTAACAAAA TATTATTTIGA	420
35	TTCAATAAAA TCAGGTAGTT TTATATAATT AATAGATTTA TTATTAACTT TATTAGTTAA	480
	ACCATTIATT AATTGATCAT AAATAATATA AAGGAATAAC ATTAATGATA TAATAGITAT	540
40	TATAGAACCA AATGAAGATA CTAAATTICA ACCTAGGAAT AGATCAGGAT AATCAGGAAT	600
	TCPTCTTOGT ATACCATTAA TACCTAAGAA ATOCATAGOG AAGAAAATAA TATTAAGACC	660
45	TAAGAAAATT AATCAGAATT GAATTGTGAT AATTTT	696
	(2) INFORMATION FOR SEQ ID NO:780:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 722 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:	
3	(A) ORGANISM: PAG1501UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:780:	
	GATCAAATAA AAATAGAAAT TAOCTTAATG GTAGAOCATT CGTTTTACAC ACGAATAATT	60
15		00
	TGAGTTOGAT TCTCAAATTT CTAAATAATA ATTAACAATA ATTTAAATTT GOGTAAAAAT	120
20	TAATAAATAT TAACGTATAT AATAATTATA TACTITATAA AATIACICAA TGITATTAAT	180
20	AAATTIATIT CITATCATTA ATAATGATGI ACCTACTCCA TATAATATAT ATTITCAACA	240
	ANTIATT CHARAITA ALAMONIOL ACCINCICCA INIAMINIAL ATTITICANCA	240
	TICACTACIA CCICATCAAG AAGGIATITI AGAATTACAT GATAATATIA TATICTATAT	300
25		
	GUTACUTGIT TUAGGUTAG TUTCUTGAAT AATAATTAUT ATTATUAAAG ATTATAAAAA	360
	TIA ATTY YUNGU (YUNGUNA ATT ATTATUM A ACA TICCUMA AATTA ATTO A	400
30	TAATCCIATT CITTATAAAT ATATTAAACA TOGTCAAATA ATTGAAATTA TITGAACTAT	420
	TTTACCAGCT ATTATTTTAT TAATAATTGC ATTTCCATCA TTTATTTTAT	480
35	TGATGAAGIT ATTICACCAG CITATAACITAT TAAAGITTATI GGITTACAAT GATATICAAA	540
	ATATGAATAC TCAGATTTTA TTAATGATAA TOGTGAAACT ATTGAATATG AATCTTATAT	600
	ATATOSATAL TONATTATA TANATONIAN TOSTONANCI AFTONANAIG ANTOTTATAT	600
40	ANTICCIGAA GAATTATTAG AAGAAGGICA ATTAAGAATG TIAGATACIG ATACTAGTAT	660
40		
	TGTTATTCCG GTTCATACTC ATGTAACATT TATTGTTACA GCTCTACATG TTATTCATGA	720
	TT	700
45	11	722
	(2) INFORMATION FOR SEQ ID NO:781:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	
	-	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1502RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:781:	
15	CATCOCTCCC AACCOCTCCT TCATCTCCAT ACTCATCTCC TTTTTTCAGGT ACCCCCGGGG	60
	CITGAATACG CACTIGICGA AAACGAACAC ATAAGAGAAT GACGCCACGA TCAGGIACAG	120
20	CAGCCAGCCA AACACTGTCG TCACCAAAAA CAGAGACAAG CTCTGCCGCA ACAGGCTGTA	180
	TOGOGGCAGO ACCGACOCGA AAGCATGOGG GCTAACCTOG AACATAAACG GTGCATTACCC	240
25	ATATACCICC ACCECCTCT CAACCEACCT COCCAACACE CECCICECAT TEACCATCIC	300
	CTCCTTAATC ATCCCCTCCT CCCAACTCCC CCCCATCTTC CCCCACACCC ATCCTCCCAC	360
30	CAGTGTGGCA TACACATAGT CGAAGAAGTA CGAGTGGCAA AACTGGAGCA CTAAATGCAT	420
	GGTCGGAGAA CGCTATAGAC TAGGAGAAAC AATTTTAGCT CTAGGTTGCC TGCCTTCTAG	480
35	CGIGATAACA GATCCIGCTA CAGCTACTAA AGCCCATCIG COGCICTCCT CIGGCITTITT	540
	GCACTITITAT ATOGTCCATC CCGGCACTGA CCTAACGTAC GCGCCTCTAT ACGACGCTAA	600
40	AAAATCAAGT TACGAATGCA CTATACGAAT GOGTTGAGCA AGGAACGAAT COCTTTTGGA	660
	ACCACCATAT CACCICAACG AACCCCCAAC GITCOGCIGC CCCCCCCTA	710
45	(2) INFORMATION FOR SEQ ID NO:782:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 692 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1503RP

	(A) ORGANISM: PAG1502UP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:782:	
10	GATCAAAAAT ATTOGAGGCA TTTGOOGCTC TTTAGTGTAC TTCGGGGTCAT TATGGAGATG	60
	GCCAATTTAC ATCOGTIATTT TCGCCTTACT CATAAGAGTA TACAGTGCCA ATTTCCGTGA	120
15	ATTGAGGCCT ATAAACATCT GGTATGTCTT ATCTTCAGTT CTCTCTGGGG ATTCGCCCAT	180
	CACTEGGAIT CCATTCAGIT TCAGGCTGCC AGGAGTTGGA ACTAAAACGT GGTTTTTGGA	240
20	TOCTOTGAGA TOTOTGITGO CATCAAGOGO AAGATAGGOA GOGGIGOTTI TGTATGAATA	300
	TOCOGUTICAS CAUGUCTCAS TOCASOUTOG AAASSTATAT TATOGUSCAA TATATATTAA	360
25	TGATAAGAGC TTTCTCTGAC TAACAGCAGT AACTCTTAAT TGAAGTATTT GTTATTTCCA	420
	ATCTTCATAC AGIATGICAC CCIGITGIAT TATAGATTIC GTTTACGAAT TOGATOGTGC	480
30	TITOGIOGOT GOGAGGICAG AAGATOGATA TAATAATATA TATATTATTA AATTATOGIA	540
	GGIAGGGAAT TOCKATITGT GICTAGIACT CGATOCCTIA TCTACAACTT CKAGITGCAA	600
35	CACATGATAT GCTGTGGACC AAAACGCTAC GCCGTTATTG ATTITATTCA AGGTCAAGAT	660
	CATATATTAG CGTAATATCT GICGAGGTTC CT	692
40	(2) INFORMATION FOR SEQ ID NO:783:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 716 base pairs	
40	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: INA (genomic)	

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:783:	
	GATCTTCGTA TACATGTCGC AAAGCTCCTC CAAAATCTTT TOGTCTCCAT CATGAGAGGC	60
10	TOCTACAGCT TITIGAGCCGA TAGAATTGGA AATACCATTG GAGATTGCTA TTAGTAGGAA	120
	CACAATATAA GTACCATCTG TCCATGGGGC ACAGGCTTTA TCAAGAAGGT CCATCAGCTT	180
15	GITCITGGAT ACAGCAGICT CATTTAATAA TAATGCCTGC TCACCACTGG GCAAAAATTC	240
	AGAAACATTG AGCAGTTCAG AGAGTGAGTT CGACTCAAAG TTTTCGGTCA TTGTCTCTAA	300
20	CAAGACAAAA ACAAGGTCCT TCCTGCTCTC ATGAACATCA TAAGCCTTGA AAACCTCGAG	360
	CAAAATAGTA TIGICCIOGA TCACGITCAA AAATACCICI ACAATTAAIG CCITCCICCA	420
25	CAATAAAGTG TCAGATTTAG GAGACAGAGT GTGGATTAAT AATGATAAAA TAACTTQCAA	480
	TICCAATICC AGCAATGICA AATACTGAAC CTTTATGAGA AGTGTAATAC ATCTGGCCCT	540
30	ACGAACCACA ATTIGCAAAAT TITTIGGATGA GGAAATIGTAC CICAATAGCA GCIGGCACCGC	600
	CTTTGTTCCC AACACAAATA ACAGATCTCG GTGTGTCAAA AATAATAATT CATAGTTCAA	660
35	TAAAACCAGT TCTAGGAGCT CTAATCCATA CTCCTCATTT ATGCAATTGC TATCCA	716
	(2) INFORMATION FOR SEQ ID NO:784:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 637 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1503UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:784:	
5	CATCTOCOCC CTTCCAAGGC AAAGGCCCCC CCCAATCCCCC AGTCTATGTT CAAGAGGCCC	60
	AACAGCAGGC CGTCATGGCA TTCAATAAGC GAATGGGCAC TCGAGCGTTG GCACATCATG	120
10	TOCTOGATAG CATCATATAC TACACAGACA AGGIOGIOGI GAAGGOOCTT GGAAATTIGT	180
	CCGCGAGCIT ACCTICCAAG ACCTCCTCGG CGACAAGCGI CAGGGGICGI GIYAAGGAAAAC	240
15	GCATTGGTCT CGAAGGCGCA AATGATGTCT TTGTATACCG CACAAAAGAC CTGGTATTCG	300
	ATAGIGATGA AGATATACCC AGAACCTAAC TACTIGIGIC GATATITICIC ACACCCCTG	360
20	GTGCGGAACC GGGGCCATAC ATTCGTTTTA CACAAGAGGG GTTGATGCAT AAAACGCGCT	420
	TICAAAAGIG GCAAGOGAGA GCIGCOGACT GICGITOCTT TIGGIGCOGC GACIGIAGGC	480
25	AATGTGCCAT CCCGTGCGCC TTCTTTTACG CGAGATCCAG TCTCGCAAGC CTGGCTGTAA	540
	CCAGAACACT COOCTGAAGC CCCCCACAGG TCCCTCGTGG ACCAGGCCAGG	600
30	TCTCATAGGC CGCATACTOG GTATCTGCCA AGAGAGG	637
	(2) INFORMATION FOR SEQ ID NO:785:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 708 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(Ari) OPTOTATA CONTINUE	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1504RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:785:	
	ርልባየ አልባጥልል ጥልልያባየንድነጥ አልርጥልልጥልልል (ደነባልያሳየልልጥል አልባናማውነማ አልባናማውነማ አለለ	60

	CIALCIGATI TIATIGAATC AAATAATATI TICITAATGA ATACTACTAA ATCATCATCT	120
5	ATTGAGTUTA TATTAAATTC ACCACCICTT ATTGATTCAT TTAATACTCC TCTAATTCAA	180
	TCTTAAAATA TICTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG	240
10	GIAAAACATA TGITTTAGGG ACATATATCT TCAGITCAAA ACTGAATATC TACATATWAT	300
	ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATOCTGA AAOCATTAGG	360
15	GGTGTGTACC TTAGCTCTCT AATTAAAGIT ATAAAATTAT CTTAACTAAT AAAAATAATT	420
	AATTAAATAA ATAAATAATT AATTAAATTT AAAAATGITTA AAAAAAGAAA TAAATAATAT	480
2 0	GTGATATTTA AATAGATCAA AATTTCAACA ATTTCCATTT CATTTAGTAC TACCATCACC	540
	ATGACCAATT GTUACATCAT TUAGUTUATU AGGUTUACUA TUAACUTUAG CUUTUACUAT	600
25	ACATOGIATI ATTOGIAATA TTTATCOCTT ATTATTATCT TTATTAGIAG TTTTATTACK	660
	AATAACTITA TGATITAGAG ATATTGTAGC TGAACTTACT TATTTAGG	708
30	(2) INFORMATION FOR SEQ ID NO:786:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 711 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
40		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1504UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:786:	
	GATCTIAATT TAAAATTTIA ATTAACTATT TATAATTTAG AAATATATAA TCTAGAGATA	60
55	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATGAAAA TTAGTAAAAT	120

	AAATAGAAAA CCATAAGITA ATTGATTCAT AAAGAAAAAT GGAATTATIT GTGGCATCIT	180
5	AATTITIATT ATTIAATIGA TTATTATCIA TYTAACATAA AACATTITAA AATGITATAA	240
	AATAAATAAG AAATTACTTA TAGAATATTT ATTAAATAGT ATTTAATTTA	300
10	TAAATATACC ATTITTATTA ATAAATAGAT TATTAAGITT ATTAATATTA AGTGATATAT	360
	AATTTAATTT ATATAAATTA TTTAATTTAC TICATTCATA TATATAATTA TTAAATGTAC	420
15	CTTTCATAAT ATTTATTTTT ATTAGTCTAG TAATATTTCT ATTTAATAGT CTACCCTTTA	480
	ATTOCATATT ACTACCIACT AAATATTIAC CIAATAATAT ATTATTAAGA ATACITAAAT	540
20	CTARTARTT ATTATCIARA GIRTATARAT TRATTRARTC TITTITTATTA TIRTTTARAT	600
	TATTATTAAT TAGTAAATTA TATTTATTTA TITTAATTAA CATAATTITT GATAATAATA	660
25	TACATTATIA AATOGIAAIT TATTAATAAT TATCITTAAT GATTTAATGA T	711
	(2) INFORMATION FOR SEQ ID NO:787:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1505RP	
	pri viva atturi. Iradijojiu	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:787:	
5 0	GATCATCTTT ATACCATTOG CICCIGITOC GIGIGCACCA ACGIAATCAA AAGOGTGIGC	60
	CCCCTOGCTA CGCAGGAAGC ACTAGAACTA GCTGAGTAAA GCAACGGTGA AAGTCGATCC	120
55	CTGATATATA TACGAAACCA GAGATACCTT CATCACAAGG ATCTTGTTCC TCGTGCCCCA	180

	AROSICACOS OSICIOSCIA COATAGIAGI TACTICICAA ACCAGACAT TOCAGGITOG	240
5	ACTOCIOCOC GOGAAGICOT TATTITITIT GITCOCTOTT GITTCAGCIT TITIGICITAA	300
	AAGGAGCAGA AAGATTATIT TGCAGCTCTC TITTGGCCCC AGCTGGCAAA AGCGAACTGT	360
10	TGATICACAA GCTTTTAACC TGTTATTAAC CACCAGCAAC CTCTCGAATT TAICATGTCT	420
	CCATCAAATA AGGATATIGC TGCCCTAATT GITGACTICC TAACTACGIC CGCCAAAACT	480
15	GIROCAGAGA ATTACGAAGA TICCCICAAA GIGGCAATIG ATTGIATCAC TGAAGCITTIC	540
	GAACTTOGAC CAGGOGAAGC TGACACATTA GTTTCCCAAA AGTGTGGGG AAGAAGCCTC	600
20	TCTCAGTIGC TCACCACTGG CATGGCTCAC ACCTCAGATG CAGGCGAACC GAAGGTAGCC	660
	OCCGAAGAGI TGAAGAACGA ACCIGAGOCC TIGAAACIGG AAGGIAACAG	710
25	(2) INFORMATION FOR SEQ ID NO:788:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
30	(B) TYPE: mucleic acid	
50	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1505UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:788:	
45	CATCAAGCIG GACAAAAACT TOOGTAACTA TOTGAACCTA CIGGAAATOG TICAGGGGTA	60
	CGIGGACCTT AACATGIAIG AACATGICIG GCCAAACCTC GITCAATTAA ATGCCAAAAA	120
50	TGAGCCIGAT AGAGTICCAG GATATIATAT TACGAGGTCT ATCTCACTGA ACCAGCTTIC	180
	CACCAGTATA TATOCTIGAGG AGTTOGATAA GTTTAATICTA TOTOCTIGTCA COGAGATAGA	240
55		- **

	AAAGAGGGIC GIGCAAGCCA CIGAGIGITT CIGGAAACIA ACATIAACAA ATAGCCAICA	300
5	TGAAAAGOOG COCATACTGA TATCAACCTT TCAAAAATTG ACAACGAAAA CTTCTCAAGC	360
	TACTITICAT CCAATGATIG ACCCAGATAC CITACTCCCT TICATCCTIC TICTACTITIC	420
10	TOCCOCACAA GITAAAAACT TGAAGAGTCA TCTAGATTAT CTTAGAGAAT TTGCGCAGAA	480
	THOSCARCAC GUARACITUG GCCTCCTTGG GUATTOCCTA TOCACGCTCG AAGOOGIGGT	540
15	COGATATITC GATATIGOCG OCAGCICAAT TAAACTIGAA AGATIGAICA CACCAIGICC	600
	AAGGAATAAG ATCTTCTOGA ACTTGATAGA GCAAGGAATT CCAATAAATT TAAAGGAACA	660
20	TGAAGAAGIC CTCATATCOC GCACTCCGIC CTGTGAATCA TYTTGTCTTT ATGIT	715
	(2) INFORMATION FOR SEQ ID NO:789:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 720 base pairs(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1506RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:789:	
45	GATCTACCOG TICOGIATOC COCTTIGAAA ATAAATTCTT TGTCTTTTGC ATGCAACTAA	60
	AATGGGATGA AGATGCAAGG GATGTTATTT TTAAGTATCT CCATCTTTTG CAGCTTTCTT	120
50	CACAGGCTGT AACATTAACA AGGTCAAAAA CTCTACAGGT TATAGAAAGG CTTTGTCACA	180
	GAAAATTAGC GTATACGAAG TOGGATGAGT CTATTTTCAG CAGCATTAGT GATATTCCGA	240
55	TIGATICGACA TGACTIGICA ACCOCTGAAA CATCTICCGA AGAGCAGCCG AAATCTCAAT	300

	CITIGITICA GCTATTIGAG CACAAAATAT ACAGCCTAAA CACCCACGCT CCTIATATGA	360
5	CTCACGATGA CCACTTCATC CAATTTGTGG CTCCTCAAAT TCAATTGAGC ACTAAGGAAT	420
	COCCCCCAAC GIGIGIOCIT GITACIOCCC CITICGATGAA ACTGAAAATT ATAGACTITCG	480
10	ATTCANATAC TICOGACAAT GAGTATWATG AAAATGTCTT TATGACGAGG TACACTGCAG	540
15	CATTGATTCA AGCAAATGIA TTTATCTTCC AAGAAAGTGA CTATAAAGTC TTTCAGAACT	600
,,,	CATTGTTTAA TOOCAAAGGC TACGGTGCTA AAAGTACAGA AAATTGGCAA CCTTGGCTAG	660
20	GACTOGAACT ATGITTICAA COGGAGOOOT TOCAAACTAA TACOGITATI AAAGAATTIC	720
	(2) INFORMATION FOR SEQ ID NO:790:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1506UP	
	(A) COSTATORI. PASISUOUP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:790:	
45	GATCTCCCCA TAAGCTCAAC ATTTTCCATA TAACATATTT GCGTCCCCGC CCAAAACACG	60
	ACCORTCOGTC CCAAACTCAA TOCCCCATTT CCAACAAACG CCAAATCATG ATTCCATCTG	120
50	TOCCTOTOGT CAATCACOGA ACTIVACAGT AGTIGACOCT TIGICACTIG GACTAGATAG	180
	TIGITGGIAA CGAAGTAGIA TATOGIGGOG CCAGOCAAGT COCTAAGGAT GOCATCAACT	240
55	TOGICOCATT CCATGICTIC TICOGAAGAA AAATAAAGTA CAAACOCCCT GGTTATGGIC	300

	GCCCCATCAG AACCAATAAC CAAATAACCT TTATAGCGTC TATCATCGCC ACAAAGTCTT	360
5	GIATACACTT CTTOGGCAAC GGCATCCAGT CCTATGGTCC ATATGCTGTT AAAACGCAGG	420
	AATTCTCCCA GGTACAATAT GTTTTTAAAA TGGGCTACAT GACCATTAGT TGATATGTTA	480
10	GACAGCACGG ATGATGAGCA AGAACATAAC TCTTCCTGTA TTGTACCTGA AATGGCAGGA	540
	GTTTTATCOC GGAAAGAGAT CAGCTCTTCC GCGTATGCAA AGCTGGTATC CTTGGTGTGT	600
15	CTTCTAAGAA TATTTGACAT AGACTCCACA TAGGCTCTGT CATCGAGGAT TGCAATGCCA	660
	AGAGAGATOT AGOGITATOT CAAATACOTT CCAAAACITA TAATOTGTAA TIT	713
20	(2) INFORMATION FOR SEQ ID NO:791:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENSTH: 707 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1507RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:791:	
40	(AI) SEQUENCE DESCRIPTION. SEQ IS NO. 131.	
	CATOCOCTOC OCTOCAACCA TOOCACCATT OCTOCTAACG GGGCTGAAAT ATATGTCGGA	60
45	CTCATCOCTG ACTTTACOCT COCCOCCCCA GACACGTCCA ATGCCCCCCA GCCTGTGTG	120
	CTGCCCATCC ACCTCGAAGC ATGCCCGTGC CAGATGCTTC TAGACCCGAT CCATATCCCG	180
50	AACOCTATCA ATTOCAGTOC AGATGOCTCG CAATTCTATC TGACTGACTC GCTAGCATTT	240
	ACCATATOGG CGTGCCCGGT AGTGGACGGT AGCCCACAAC TCCTCAAGAG AACCCCATTC	300
55	TACTICTACCA AAAATACTICG CAATGACTICA CACACTTOGC COGAACOOGA TOGTICGATTT	360

	GIGGACIGOT TRACIGOSCA CACTITICGIG GOOGIIGIGGT CCACTIGGCAA AGTCCGAGAA	420
5	CTCGACAACG CAGGCAGACT ATTCGCTGCA TATACACTAC CGACGCCACG AGTCAGCAGC	4 80
	TGTTGTGCGG GCCCCCCAGG CGAACTGCTC CTGTCCAGGG CGCACGCAGG CGAITTICAAG	540
10	ACTOSCOCAC ACTOTOACOS COTOGGAGOS AGCATTITOA CACTOGTAAT COCOCOCOC	600
	CGCGPTATCC CAAGCCGCAT CCCCGCGTCT TGCGGAAGCA TCCTTTAAAT AATATTTACT	660
15	TCTACACCCT CTCGTCCCCT CTACCCCCCA GCTCATTGAT GGGCCGT	707
	(2) INFORMATION FOR SEQ ID NO:792:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 570 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) Original source:	
	(A) ORGANISM: PAG1507UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:792:	
40	GATOGRACCA GRATAATACT GOGAATIGAC GOGCOCAGOO AAGGOGTOGT AATOATOGTG	60
	CTGATAATTA TGTCCATAGC CATCCATWAT GCAATTAGCA TCAGCTATTT GCTTACGGTG	
		120
45	TIGACGAGCG ACTIGITIAATC TCCATAGAGA ATTCTCCTCA ATAATTTCTIG AGACWGTCCT	120
45	THE ACCACION ACTIGITA AT COCATAGAGA ATTUTOCICA ATA ATTUTO CACACACIOCTA ACCACACIOCTA ACCACACACITA CACCACACACITA CACCACACACACITA CACCACACACACACACACACACACACACACACACACA	
45		180
	CHTHTHAAA ATCGGCTITG GCCCCGGACG TIGAGGGGGG CCAGIGCTAC CACCAGACTT	180

	ATTATICCO COTTIGOCCO ALCICCICCA GEATIGORITO TOTACOCCO CONCENTOAC	480
5	GAGGICCIOC TCTCCCITCT GICTCTTCTT CAGGAIGAIG TACTTCCAGG ACTGAGAGAT	540
	GTCTCACTCA GCCCAGTCGT GCCAAAGGTA	570
10	(2) INFORMATION FOR SEQ ID NO:793:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 692 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1508RP	
25		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:793:	
30		
	CATCCACAGE CAAAATTIAT GCATATAGCT TOCTTATATT TATGCGGTGG ATTCTATATG	60
	TOGCACGCTA AATWCTAATA GOOGCOGGIA AAAAGTAGTC CTOGGCAAAC TOGGTAACGG	120
35		100
	CAAGGICGGA ATTATAGAAA CGGGACTCAG AAAAACTAAT CCAGAGIAAT TAAGGGACTC	180
	GCAAAGOGGA GCCGGTTCTT ACCGAAAACC TCAACGGAAG TATATGAAAA AATTTATCCT	240
40		
	GCAGATTATA CCCATGCCTG TTTTATCCAA GGTAGCCCAA ATATATACTA CAGGAAATGA	300
		•••
	GIGACTITIC ACTIOGAGAG COCAAATAAC AATAATTITA GIAAAATTIT AGCATTOCTG	360
45		
	CTACTOCAAC TITICCAATGA ACACTICIGA AAGOGTAAAT ATATAGCTAT GOGGTTIGOC	420
	TCCCAGGCTC TAACTACAAA TTCCACCTTA TGTGTGTTAT TCAGGAAATG CAGGGGAATA	480
50		
	GTTGAATCAA CGAAATAGCG TTAATTTGCA ACCCCCTTGT ACGTGTATAA AACCCACCCC	540
	CCICCGAAAA AGATGACTAT CGITATAAAC TAAAAAAACAT CATCAAAAAA GAACTAAGIT	600
55		

	ACTGAAAAGA AAATGGTTEA CCGTCTAGCA GTGAATTTCA GCAACCAGCC CACATGOGTA	660
5	ACCAATTICC GAATCIATCG TIGCAGAATA CT	692
	(2) INFORMATION FOR SEQ ID NO:794:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI508UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:794:	
30	GATCIGGIAA CGACTAAATA AGAATOCTTA COCAGCAACG CCGGCGGGGT CTCGGCAGIG	60
	TAGIGICICT CAAGIGUOG TCTGOCACTA GTTAGGICTT GCAGGITGCC TTTGAACCAG	120
35	TOCOCCIOGO TAMOCACOGA CATODOGGAA ACTOCOCCOT COCCATATOC AMBOGOCTOT	180
	TOTOCTOCAA GOGCOTOGOT AATATTOCCA COCCACOGAG ACOCACGITT TATCTOCOCT	240
40	ACCACAGOCA GCCGCGGGG GTCCCGCGCC AGCCGCTCAT GGAAGTCCAC CAGGCCGGGC	300
	AGAACOCCCA ATCGAAAGCT COCCTCCAGG TCCGCCATAC CAGTTCCCGG CATAGCCATC	360
45	TECCCTECCA CETCCTCCTE TOCTTCACCE TATATCTCCC TCACCACACA CCCCCCCCCT	420
	GCCCCCAGCT GCAGCTTGTC GTTCTCAGCC CACGTACCCC CTTCCAGCGC TAGCATGTTG	480
50	COCACCATTA OCTOCCOGTO GICCOGTCACA ATCCACTICCO GGIGGAACTO CACACCCTICC	540
	ACCEPTED TO TO THE PROPERTY ACCEPTAGE TO TO TO TO TO THE PROPERTY ACCEPTAGE TO	600
5 <i>5</i>	TCCAGCTCCG CCCCCAACCT TCACCCCAGT CCAGCCAGCG AGTGCTACCG TGTCACTGCC	660

	ACCOCTICAC TACCOCTICA AGAACCOCCC CCCTCCTCAC CCACCTCCCA CCTTCT	716
5	(2) INFORMATION FOR SEQ ID NO:795:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1509RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:795:	
	CATCCAGITT CTCTCCCATT TTCTCAACCA TGAGATATGA GTCTAAGTTG GCTAGATTAC	60
30	TATATAGCCA GTTGTTCGCT CCACGGGCCA AAACCGAGAC CGGTTCCTTC CTTTGACAAG	120
	AAGAATAATC GCCATCIACT TIGITIGAAT TCTTTAAACC GICIAACICT TGCAGIACOG	180
35	TITTIGGIAC TACTATGCGA TAGCIGIATI TIGGGGCAAG CACTCGIAGT TCTTCAAGGA	240
	TATOCAGATG TGATAACACA TAATTAGTAT CAACGACCAG TGCAATATTA TGCAAGTCTT	300
40	GOOGCACTIC AACCIGOOGC TGAATTACTT TTGCGAAAGT CICTTOOCCC GGAATATCGA	360
	CICICITGIC AGGAATAGIC TTAAIGITGI TAATTICAIG GCIGICATAT TOGICIATAT	420
45	CCATCATCCC TICACCTICG IGITCCCTTA TAATTICTGC TICAACCAAT GCATCCAATT	480
	CTGCAATGCT ATATTTCTTA TTAGAGTGCT TAGGGTTCCA AGTATCCGGC GAGCTTATGG	540
50	TATOCCICIT ATTCICATOC CIACOCTIOC TCITOCCCC ATGCICCCIA GACATCICCT	600
	GIGIAGCIIG GIGCATAGAC IGIATATGAT IGGACTCCAT CGGAACTAGI GGCACGITTA	660
55	AAAGACAITA AITAGGIATC ACCICCAITA ACGIACCITT GATATITATT ATATGA	716

(2) INFORMATION FOR SEQ ID NO:796:

5	(i) SEQUENCE CHARACTERISTICS:	
3	(A) LENGTH: 590 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDFINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1509UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:796:	
25	CATCTOCAGT TICATCACCA GIOCATOCAA CATGIGITTIC TAAATICCAAC TAAGGICCGT	60
	AMBGICAGIG AGGIGCAGIC CITTATCACT CIAAAATTCC CCICTTCCTT TGATGATGAG	120
30	ATACTOGAGT CATOGATOCC AACTACAAGT CACCATCAAG ACTTAACAAC TCAAGACGTA	180
	CTTOGTOGAT TOGTOGATOC TATOGATOAT AGGCGCGACC AAGAAGACGA TATOGATTOG	240
7.5	CAACAACOCC TOGATGIACT TOCTTIGATIC GOCTGOGACA GTOCAGTTTC CAACTTGCOG	300
	COGNITACOS GOSTICCTOS TICOGNOCAT GOAGACCAAT GOGNICTICO ACAGACCAGT	360
40	ATTACTOCTA ACAAACTAGA AATOCATTOG GIOCAGAGGO CTACCACACA COGIGIGOGGI	420
	GIGCTAGAAG AAGAACAATC GCCTTTGATC ATGCTGCAGA AGCGCAGACT AGCCAGGAAT	480
45	GGGTCAAGAA CAITAGCCAC AGCTACAATC AACCATGACC AGGAACTGCA ACTAGAAGTG	540
	CCAGATAGAG AAGCCGCTTC GCCTGCCATT GAACACGAGC AAGCCACCTC	590
50	(2) INFORMATION FOR SEQ ID NO:797:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 723 base pairs	
55	(B) TYPE: nucleic acid	
	(C) STRANDETNIESS, cincle	

	(b) forologi. The	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1510UP	
0		
	(ad) CTOURS TO DESCRIPTION CON TO NO 707.	
15	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:797:	
	GATCAGAATT GGAAGGGATG TTTGOODGAA GAAGTTOGTG ATATOGAGGA GOOCACTATA	60
	CCCGICATIG GCCGGAAGIT TITCAAGIAC GAATCICCTA TAAAGCACTT GCTACCCCCC	120
20		
	AACGCCACTA TAAACGACCC CATTOCTCAG CCAACTGAGG GAGCGGTCAA TGCTCCACCA	180
25	TIGGTIGGGG CCGITTATCT ACGCCCAAAA ATTAAAAAGG ACGACTTAGG TGAATATTCC	240
25	100000000 100000000 company 100000000 100000000	200
	ACCTCOGATG ATTIGTCOCAG GTACATTATC AGGOCTOGTG ACCCGCCTGA GGTTGGTAGA	300
	ATOGACOCAG AAACGGGAAC CATCATTACC AATTICCCAGA COGCCAGTGT ACTACCGAAA	360
3 0		
	ATGAATATGT CTACACCACG TCTGTCGTCT TTGAACCOCA ACGGTACCTA CTCGAATTTG	420
	ATAGGCCGIT CCGGTAGCCC AATTAACATG ACCAGGTCCA CCCAATACTT CGCACCAGTT	480
3 5		
	CCTAACGGCG ATCTGAGAAA TCTGCCAATC GTGCAACAAA TACCGAATAG CACTATCCCA	540
	MOMOCOCKOR OCHUMOCKA ACCOCCONANA CLOCOCCOLOCA ACCOCCONANA CALVURANA CAL	606
40	TCTGCGCAGT CGTCTGCAAA AGGCGGCATA CAGGGGGCACC ATGGGGGGTT CAATTAACGG	600
	TACTACCOCT GCATACCAAC CCCCTTCCAT TATTAATAAC CTAGCCGCCC AGGCTAAGAC	660
	AAACAATACC GITCTTGGAA ATATCTTGGT CGATACGCCC GGTGCCTACG TTCTCCTATA	720
45		
	TCT	723
	(2) INFORMATION FOR SEQ ID NO:798:	
50		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 693 base pairs (B) TYPE: nucleic acid	
55	(C) STRANDETNESS: single	

(D) TOPOLOGY: linear

5	(11) MULECULE TYPE: DNA (genomic)	
	(vi) Original source: (A) ORGANISM: PAG1510UP	
10		
15	(xí) SEQUENCE DESCRIPTION: SEQ ID NO:798:	
	CATCOCCOCT ACTOTICTAC GACCACOCCC GOGGOCTGAA CCTGGCCATC GOGTTCAACC	60
20	TOGAGGACCC GCAGGGGGG GGGAAGGAGC GGGGCTACTG CCTGGTGCTT ACGGTGGAGC	120
	TOCCACAACG GOCGCCCCCA ATGGAGATCC TGTCCCAGCA CTGCAAGTTC ATCTCCGGCCC	180
25	CGTTCGAAAA CATGATCGAG TACATCAAGC AGCAGCGGG CCCGGAGCTG CTGCCGGGTGA	240
	TOCASCAGGE GCAGGIGCAG GGCACATOGA ACTITITOGIC CATOGICAGO GGCACCITATO	300
30	TOCOCCOCAA CAACCICAAG ATACOCGAAGA ACATCACOGA GCICACCAAC GATAGACTOC	360
	TGITCGTCAG CATACACAAG TGGAATGCAT TTATACTGCA TAGACTGGGA GCGCAGCTGG	420
35	ACTIGAACCCT TGGGGGGGTG GCTGGGGGGGC AACAGTTGGA AGATAGAAGA CAGAAACGCC	480
	COOGNAGCCG AGGCCGCAGG TCGCAGGCGT TACATAACTT ACATTCTTAA CTAGATAGTG	540
40	TICOCCIGIA CATCAAGIIC AGACGITAAG GIIGAACOOG OCATOOGIGA TGIGIICOCT	600
	CAAGGGGGCC AATGCACATT TCACGTCCTT GTTCATGAAC TTCTCCACCT GCTGTGGGGC	660
45	CCTGCCCACA AACCTGGAGG GGTCCAGCAG GGA	693
	(2) INFORMATION FOR SEQ ID NO:799:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 676 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDELNESS: single	
55	(D) TOPOLOGY: linear	

	(11) MOLLECOLLE TYPE: UNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1511RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:799:	
15	GATCGACCAG CTGGTGATGG ATAGGCGGCT GGTGCCGCTG GGGCGCTTCG TGCGGGGGCCC	60
15	CONTITUES CIGITATICST COCICACETE CACCCTOCAC AACGTOCTOC ACCTGTOCTC	120
2 0	CAGGAGCOGG GTGCGGGAGA ACGGACGGTIA CCTGCGGGAAC TGCGCATIACG TGAACATGGA	180
	COTOCTOCCO COCCOCCIOCA COCCOCCIO CAACAAAAAC TICCTOCCOCC	240
25	GOCGACGOCA TATACOCACC TIGIGITICIC GOGOCGACGAG TICIACOGOG TGGTGCCGCGA	300
	GASCCTACOG OGACOCCOGG AGTIACCATIGT COTOCTOCCG GACCTOCCACA AGCACCOCAA	360
30	GEOGRATICIA GIEGACOGAG ACGITIGICAA GEIGGIGATG COGGGGGTIGC GCGCGGTGGT	420
	GCAGCCGITC GGGCCTGACC GCGTGACCGC AAACGACCGC CACATCGCAG AGTTCAAGGG	480
35	CTOGCTGOGA TTGGTGCAGC GGCAGGTCCA AGGGATCCAC GGGCACGTCG AAGAGACAAC	540
	CCCCCCCCCCC CETTGCCCCC GTCCCCCCCCCC CCATGTCCAG CCCCCCTACC	600
40	TGCGGATGAA CAACTCGCGC AGGCCAGCCT GTCTCGCGGG CTCAACCAGT TTACGAACCT	660
	AATGGAGATC AAGGAC	676
45	(2) INFORMATION FOR SEQ ID NO:800:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: INA (genomic)	

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(A) ORGANISM: PAG1511UP

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(xi)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:800:
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CATCHIGCCC CACGGCCCCT COCTCAACHT CCCCCCGTCC GCCACAAACG CCCGCAACAT

GCCGTCATCC ACGCTGGGCT COCTCCACGG CGTCTCCCCCA GTCAGCAGCA CAAACACAAG

CACTOCOGCA GACCAGATGT COGCOGTGTC CGCGGTGGTAC GCCCGCTGGC CCACCACCTC

CCCCCCACC TACCGCAGCG TCCCCCCCCC GTCCCCCCCC ACCCCCCCCC TCCCCGTCCCC

CCCCCCGAAC CCCCGAACIC CCCCGAACIC AGGITCCCCG CCCCCTCCAG

CASCATGITT TCCGGCTTGA TGTCCCGGTG CGCCACGCCG CACGCCTCGT GCAGGTGTGT

CASCISCOSC ACCASCISCI GGIAGIAGAA CGCCCACCT CCCAGICCAC CCCCACGICC

COCTOGATOT TGTOGAAGAG GTOCCCCCCG TOCCCCAGCT CCATCCCCAT CCATACGTAC

TCACGICACA CATTGCAGTC CAGCACCCTC ACCACATGTC GGTGCCCGCG CACCGCGTCT

GCAGCACACC TCGCGCGTCA GATCCTCGTC CGTCATCCCT CGCGCTTTGC ACCGCTCCAA

GTGCACCAAC TICACAGCCA CTATCGTCTG CGGGTCTGCG CGCAACGAAG CGGTTTTGAA

GAACGCAACG TGCCCTGCCC AATOGTCTCC CGAAGCTCTA ATTCCTTAAT CTCCGGGAAG

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(2) INFORMATION FOR SEQ ID NO:801:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 base pairs

(B) TYPE: nucleic acid

(C) STRANDELNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genamic)

(vi)	ORIGINAL	SOURCE:
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(A) ORGANISM: PAG1512RP

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(XI)	SELUENCE	DESCRIPTION:	SEV	щ	MO: OUT:

	_	
10	CATCTTCACT CCAAGCATGA CCAGCAAAACC CCCCACAGGG CAGAAAACTCC TATTTCCCFIG	60
15	TCTACACCOG CCTCTACTOG CATOCAAGIT TACCTATACC TCCACTATTA CIAGATATCT	120
15	ANTOCCTACC ATATGITGIG ATGACACTGA CATTCAGCCT TTAACCACTT CAGCTTATTA	180
20	AAAGATTCCA GACATACAGA AAAAATCCGG TGTTAAAAGT TATACATATA CACCATTTTA	240
	CCTATATACG TGTAGACCAG TAGAGCTACT AAGCAGCCCA AGAAACACTA CCATATTCAT	300
25	ANTODOGAGO CTANOGACTT TOGATIGOGIT COGIATGIGO COMOGUTIAT AGIGCACACA	360
	OGATISCAGITA CTAACAGITOS TAGCAAAAAC OGACCAGCAG CACGITOCGIC GGITCATICTOG	420
30	COCCOCCATT ATCTCCATAA TGATGIACCT GITCCTCCTG TTTATCCCCT GCCCCAATT	480
	TOGCASCIAC TITIGGOGGCT ATTIGGACGA ACAGIACATC ATCGACCCCG AACTGCGGCA	540
35	GACAACGCAG ATTAACATGG ACGTGATGGT GCAAATGCCG TGCAAATACC TCGACGTCAA	600
	GOCAACTGAT ATTACCAGGG ACATTAACGA CGTGTCGAAA AGACTGGTGT TCAAGAATAT	660
40	CCCTTTCTTC GTACCGTACG GCACCACATT TGACTCTGTT AATGAGGGIC CGCACCCCGG	720
	AC	722

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(2) INFORMATION FOR SEQ ID NO: 802:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 679 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEINESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

	(A) ORGANISM: PAG1512UP
5	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:802:
10	
	GATCGAATOG CATCCCATTC ATCCGATGAG GACGCTATGT TAAATAAATA TTATCTATAT
	ACTOTAAATA CTATATOGIT TCATCOGIGT TACCOGCATT TAGAGATOGG CGITCTGGIC
15	
	TOCAAGCTIT AACTOGIGIG GCTGACGATT CTACATAACG TGTATTGACC AGGCTGAGCA
	GIAACGITAG CAACTIGGAC ACCAGITATG AGIACCGATT TOGACAGAAT TIATTATIAAC
20	
	CAGTCAAAGG TGAGCGGTGG CITCCGFTTIG GGCGAAGGIG GCCTGGGATG GAAGGCTTCC
	GCCACTGGGG GGTCGGCTGC CATGCAAAAC AACGAACCAA TTCTCTTGAC TGCGGACGAA
25	CTOCCTTCCG TGCAATCGAG TAGAGGGTCC CGTGGCTACG AACTAAAGAT TAACACGAAG
	MATERIAL CONTROL CONTROL AND TANGACTAGE
30	AACAAGGGG TGGTGCAGTT GCACGGTTTC TCGCAGGAAG ATTTCACATT GTTAAAGAAC
	CATCTOCAGO GCAGATTCAA CGTGCAGTTG CAACACAAGG ACCACTOGOT TOGGGGATGG
35	AATTGGGGTA CTACCGATCT GACAAGAAAC GAGCTGATCT TCTCCCTAAA CGGGAAACCA
	ACTITOGAAA TACCATATIC GCATATCAGI AACACGAATI TAACATCAAA GAACGAAGIIT
	COCCUPANT TO COLUMN TO COL
40	GOGCTGGAAT TOGACTTGC
	(2) INFORMATION FOR SEQ ID NO:803:
	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGTH: 721 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEINESS: single
50	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1513RP

(vi) ORIGINAL SOURCE:

(xi)	SECUENCE	DESCRIPTION:	SEO	\mathbf{m}	NO:803:
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5	GATCAACTGT	TOCTCCAGTT	GCTCCTTGGA	CTIGGITCIC	AATTCAAAAG	CTTTAACACC	60
	GECCTGAGAT	GAGATGITAG	TACTCCGCCC	ACCUATCAAG	CTTGGAATGA	CATTOCTOOC	120
10	AACCTGCGGG	GCCGCATCTA	CCCCTCCCCT	ACCOCTOGCT	GGCTAACCCG	GIATOCCCIG	180
	CTGTCGCCCA	CLICIGICCC	ACGGATTTAA	GCCTCTAACG	GTCACCTCGA	TACCCAACGA	240
15	AAAGCTGCAT	GCCATCATCC	CACGCTATAC	ACCCCCTCAC	ACATACCATT	ATGATTGATT	300
	TIGCIGIATT	TIGCACTAAG	AGCCACTCCA	AATGAACTGC	CTCTTCTGIT	CAACATCTTG	360
20	CCCTCCTCTG	GAAACCGACT	GIGCICCGCT	CGC7G7GCCC	GAGCGAGICT	GTCGGACGAC	420
	GCAGAATCTT	CAGCTATACA	ACCCACACAC	CTCCGAATGT	ACCGATCCAA	CAGTCAAACA	480
25	CAATTCACAA	TCACGTGACC	TACAGGIGAA	ATTAACGATT	TOGGCAGATC	OCAAAGTGAG	540
	CCCCAAAGCC	GCGACGGAAC	ACCOGGAGCCCG	GTACACGATG	OGIOCCACIT	CITACACTAT	600
30	ATATOGATOG	TAACAGIGCA	COCACAAAAA	AAAGTAGIAT	ACTAGOGICT	ACCACACTIC	660
	GCTAGTTCAT	TTACAGCCTA	ACCTAAACAT	TAATTATOCC	AAGACAGTGA	TTOCANCONG	720
35	A						721

(2) INFORMATION FOR SEQ ID NO:804:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1513UP

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(XX)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:804:
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5	GATCTTTAAA ATTTOOCAAG AACAGCCAAC ACTCCCGTCA AAATAAAGAG CAAAGCCCCT	60
	CCACACCTCT ACGAATCAGG TCCGAAAGGC GATCTTGCAA TGACGAGCAA GGTTACAAAG	120
10	AAAGTTACAG AGTOGCACAG TGCATGTGAC GACCAGCAGC ATAGTTCTCG GOCTCGCGGC	180
	ACTOCAGCAG AGGGAGGOC TAGTAACGTG GTTCAACCGT CCCTCGGTCA TTTGAAGAAA	240
15	CTCGCAGAAT ACACACTCTC CACCOCTACG TCGAACGAGT GCATTAATAA ACGGCTGCGG	300
	TCCACGAACG TGCAGGAGGT GAAGCTGGGG GGACTGCAGT TTCTGTTTTA CAAGACGCTA	360
20	CTACTGTGTC TTTACATGGC ATATGGGTTC TACGGATACT TCCAATACCA GTACAACAGG	420
	CIGOGTATCA AACTACICAA TCIGGCCTAC TCGCCGICCA ATACCCCGCA QCIGATCAGA	480
25	CAGGACGIGC TAAAGITIGCA CAAGGICCCT AAGCGGCTIGG CAGCGATTITT GGCATACAAG	540
	TCTGAAGGG AGGTCGCCG TGGCGTCCAC GGCTTGATAA ACCACGGAAG CAACGTANTA	600
30	TOCTOGRACIE TETCTOCORE CATCARCERC CTETCOCTTT ATGATICATGA CORRESPONDE	660
	AAGGCCAACG TGCACCAGTT CCGCCAGGGC GIGITACGATA CCIGGGGGCC TACTACGGCCC	720
35	CAACAA	726
	(2) INFORMATION FOR SEA IN MOURAGE.	

(2) INFORMATION FOR SEQ ID NO:805:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGIH: 736 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1514RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:805:	
5	GATCTOCGTG TATATTTOGA TOTATATOGA CTTCACACTT TCGGAAGCAA TOGAACTCGA	60
	ANGCIGGITG ACCACTCIGC IGIATICICG TAGICITICI GAAACGACGG TAAGAAAAIT	120
10	AACCITGAGC GOOGATAGGG AAGATGCAAC TITAAATITC TCTACTTGGT TACTCAAATA	180
	CTGATATAAT AATGCAGCCT CAAATATGCT GTGGAAAACA CCACTTTCGC CGTTCGGAAC	240
15	ATTIGGGTIGGG ATTITOGATIAA CCTGATTIGGA GATCGGGAAC AAACTGGACG TAGTAGGCAG	300
	TAACGIGIAG GAAATATACT TTAAAAACGIC GOCCICOOGC ACCAIGITGC IGIAGIAIGG	360
20	GITAGACAGA TATOCCAATG GAGTATOGTG CTOCTOCOGC COCTTOCOGCA CCCCCCCCC	420
25	GTATGCAGAG GTTACCGCCG ACCGCCGCTC TCAAAGCCGC TCCACATTCT CCAACCACTC	480
25	TGCATAGACA CTAACCOCCC TCGACCOCCT CATCAGCGAG TTGTGCCCGTT GCAGCGTGCC	540
30	GITTOGTAAGA TATTCCAGACG CGGTGCGCCT GTGTCGGAAG GGCGTGCTCT CCTGCGGCAC	600
	SCTUTTCASC ACCUTCASCAL CISCIOCITIG CTACCGAAAC TCTCCASCAC	660
35	THTCACGAAC ATCTOGAACT TCCCCCCACTG CTGCGTCTGC TCCCGCGTCCC GCACCATCTC	720
	COCCCOGTAC ATOCTC	736
40	(2) INFORMATION FOR SEQ ID NO:806;	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1514UP	

(xq.)	SEQUENCE	DESCRIPTION:	SEQ	ID	NO:806:
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5	CATCTCCACC GCGTCCACCA CC	CACGATCOG GTCACCGTCC	CACCGGGTCA	TOSCOACIGI	60
	CCGCGCGACG CTTTCGAAAA CC	CECCCETCC CTCCCCCCTC	CAGCCCCTC	CCCCCCIGIC	120
10	GIGOGICOGG TOCTOGGCCT CO	CCGCCACCG CAGCGTCGCC	ACCACCCCCT	CIATATTCAC	180
	OCCOCCESC TICASCEIGT CO	SCOCTIGAT GCCAGGGCTG	GIGGGITICT	CTCCCACCAC	240
15	CTCCAGGCTC TTGATAAACG TC	OGTOTTAAT CACCTTAAAG	CICCCACTAT	GCCCTTGCG	300
	CCCACATAGT AGCGTCAGCG TA	ATOGITICO CCAATOGIAC	GOGTATATOT	TECCTCTCT	360
20	TACACCGICG AGGACGITGG TO	CACCOGCAC CTTGAATCCA	AGGATATGIT	CCAAGTTGAT	420
	OCTOATTOTG CTCACTTOCA AC	SCOCACACA GCTATOCTOG	CCACCTTAGA	ATGCCACGCC	480
25	TOCTOCCOGTI OCACTOGOTIG AC	CTCCCAATC GTTCAGTTTG	COCIGICOCT	ATTTTTTGA	540
30	AGTOCCCTC TAGCCATGAA GI	DAGATTT CTATGUATUA	. CTATGTCCCA	CAAAGGTTAG	600
30	TTOCAATAGI GCITGCAACT A1	CAGGICCI CICCACITOC	CAAGCAGACG	ACTICCICAT	660
35	AGTOCAGCCG ATAGACAATC CC	SATAAACAT TATTOCOGAA	AATCTAACCA	CAGGTGG	717
	(2) INFORMATION FOR SEQ	ID NO:807:			
	(i) SEQUENCE CHARAC	TERISTICS:			
40	(A) LENGTH: 71	l4 base pairs			

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
- 50 (A) ORGANISM: PAG1515RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:807:	
5	CATCCTTCCC CCCGTCGTCA AAGCCCCCGAT AGGATATCAC AGGGCACTGT CCAAAGGTAT	60
	COCATATIGI TICCATGACC GITTCGCCCT TCGGTCTCTT CGCCGGCTTC CACITGCACG	120
10	19300300AG GAGOTTACAG AGCTGCAGAT AGTTATTACT GTCAAAOGTC CAGGGTGCCC	180
	COCOCCOTITT GTGCCCCCCA GCAGCATCCCG CGAAGTGGTC CAGGTGCCCC CGCCGACACAT	240
15	GGAACCOGIC CATGGGCACC ACCICAGCIA TATTGACCGA TGACGCTGGA TCCAGGGCTT	300
	COCTOCCCAT GOOCACCGAA TIGOOGACCC COCCOCCCC GAAGATAACT GOOGTCCCAT	360
20	CCCCATCCTA GAACTIGICT GOCTIGAACC CCGGGTCCTC CACGIGCGCG AAGAACCCCC	420
	GTCGCCCCTC CTCGACCACG GCGCCTCACG CAACCGGCAC AGTCTCGTCC AGGCTTTCCCG	480
25	CAGCAATGCC COCCGAAATC CTCAATCCAC CCCTTCCTCC CTTCAGCTGA CTCTGCAATT	540
	CCTGGTTCAG GTCCCGGCTTA AGCCTCTGCG CCATCGTAGA CTTGCCGGAC CCAGGATGCC	600
30	CCACCACCAC TACAGOCACC CGATAGTTGC TCTCGATATT CTGAGCAAGG AGATCOCACA	660
25	CTCCCTTCTT TAAGTCTTCG TAGTCCATCC CGCTTCCTGT GTATCCCTCC TCGT	714
35	(2) INFORMATION FOR SEQ ID NO:808:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 725 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1515UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:808:

	discrete cichards discrete cichardic igiaicider	60
5	AGCTICAGCA TIAAAAAACC GTCCAGAGAA TIGGCTITTCG GCCATGCTCG AAAGCTCACT	120
	AGTOGGAGOG CAGCATOTAG GACACOAGTA GGATGCAGAC AGTGTTTAGG CCATTGAGAA	180
10	GIGIGATICT GACGCCCCCT CGAGGCCTGG CGCGGTCCAG CAGGCTGCAG TCGGGACACA	240
	ACAAGIGGIC GACGATCAAG CACGATAAAG CGAAGAACGA TOCTGAGCOG AACAGGCTTT	300
15	TCACGOGGAT GGCCAACCAG ATATCGGTGG CAGTCAAGCA GGGCGGGTCT GCCCACCCGA	360
	COCTGAACCT GCCACTGGCG GCGGCCGATAG AAGCCGCCGTC CAAGGCCCAAT GTCACCAAGA	420
20	AAGTGATGGA AAAGGCAATC CGCAAGGGGG TCGGCGAGGG TGGGGGCGC GACAAGGCCG	480
	AGOCATOCAT GTACGAGGCG ATACGGCCCG GTGGCCTGGC GTTTGTGCTG GAGGCCTCAC	540
25	CCACAACAAG AATCOGACOG TGACCTOGTIA COCOCCOCGT TCAACAAGCA TGOCGGCAAC	600
	ATGTOGOOG CTCAGTACTT CTTOGAGOGC CGCGGGTACG TGCCAATCCA GCCACCGGCC	660
30	TOGTGCCACA GITACAACGC GGTGTTTGAG GITGTGTGCCG AGGTCCAGGG CGTACAACAA	720
	CTGGA	725
35	(2) INFORMATION FOR SEQ ID NO:809:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 687 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1516RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809:

	CATCCCACCT TIGGIGOCTT GOCTCGAGIC TITICTICAAT TIAAACCCCT GITCAACAGC	60
5	ACATCAAATT GITAGTCTAT CGAGTCCACG TAAAAGACAA TTTTCGACGC TIGAGATGAA	120
	COSTIACOCCC TCTCCCCCACA ACCOCCATOG CCTGCACCGA AAAGTATCCG GTCACTCCTT	180
10	CATCATACOG TACCTTCACT ATCTCTTTCC GCCGGAAACT AAATACAGAA ACATACCTTT	240
	AACATOCTTA TICTGTTTAT CCTTTCCTGA TITTCGACTGG AATGTAGOGG CGAAAGGGAT	300
15	CIGITICAAA AATIGGAAAC OCITACCACC TCACCAACAC ACCAGGACTT TATTICGTAG	360
	AAACAGGCGA TOGGCCTGAA CAACAGTCAC TAGAAACGGT GCACCAAGGC AGCTTGGCAA	420
2 0	CCACCACCA CCCTACCCCT CAATCCCTTC ATAGTAAACC ATGTACACCA CCTTTCTCTC	480
	OGAGAGAAGG AACGACGTCT TOCACTCOGA CACGTACGAA TCTGAGATAC ACCACCACGG	540
25	GTGCGTAGTG GTGCCACGTA AAGCCTTCAG TTTGCGGGGCA CGGCCTGGGG ACGGGGGAGT	600
	ACTIOGROC ACCOCAACAT ACCOCGATGA GCTOCCAGAG CTOCCTOCGG ACCTGTOCTG	660
30	CTOGGCTGAC GCCTCCGCCT TGCACAC	687
	(2) INFORMATION FOR SEQ ID NO:810:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) optotal compa	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1516UP	
50		
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:810:	
55	GATCATTAAC GAAATTCTTG TGGTTGATTA CGATGTTCGA TGGGAAGATA TAGCTGGTCT	60

	TACAATAGCA AAGAAGTGIT TGAAGGAAAC AGITGITTAC CCATTITITGC GGCCAGACCT	120
5	TTTTCCCCCT CTCCCCCCAAC CTATCTCCCC CATGTTGTTA TTTCCACCTC CACCAACACC	180
	TAAAAOGAIG AITIGCCAGOG CCGITIGCGAC IGAAITOGAAT ICAACITICT TITIGCATCAG	240
10	TOCTTOCTOT TIGHTATOGA AATACTTOGG TGAGTOGGAA AAACTTGTCA AGGCCTTATT	300
	TTACCTAGCC AAACGCTTT CCCCCTCAAT TATATTCATT GACGAAATCG ACTCTCTACT	360
15	AACTAGCOGT TCAGATAATG AGAACGAATC ATCCAGAAGG ATTAAGACGG AGCTCTTGGT	420
	CCANTOSTOC TOCCTANOGA GOGCCACGGC TANGGANACA AGAGANGGCG AAGAGGCCAG	480
20	ACCCGTTCTT GICTIGGCCG CAACCAACIT ACCGTGGGCG ATAGATGATG CTGCTATTAG	540
	ACGITTITICA COOCGICTAT ACATTCCATT OCCOGAATAC GAAACAAGAC TGTATCATTT	600
25	GAAGAAGCIT AUGGCCCITC AAAAGAATGA ACTTICIGAA TCTGACTTTC AACTCATTGC	660
	TOGCATGACT GAGGGCTACT CGGGATCTGA CATAACTGCT CTTGCCAAAA GAAGCAGCTA	720
30	TOGA	724
	(2) INFORMATION FOR SEQ ID NO:811:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 710 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(VI) ORGANISM: PAGI517RP	
5 0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:811:	
55	GATCAATGAA AAACATGCAT ACGATTTCAT GAAGCAAAAT TTGGCTTGGA ATATTGCCAA	60

	CTCTATTCAC AAAACAGAAA TACTAAAGGA AGAGAACTTC ACGITATTAT CCAAAGCCCA	120
5	AAGAGATGAC GTGAAAGGAA GAGAAGCGGA GITATTACTT CCAAGGGAAT TAAATCAATT	180
	AAAGATGGTC AATGAGCGTG AGCTGAACGG CCATGCAAGA AAAATAAGAC TACTIATCCAT	240
0	GTGGGAAGIC TTCAAAATGC TTTAGGTTCT GCATTATTAT ATACACATTG TAGATACAAC	300
	TOGARACTAR TOCATTICAC GTCACCAGTC TARRAGTOGT CATGURGIAR CTTCACACCT	360
15	TOTTTATTOC AAGGACAAAG GTATATTOCC AGCTGTGTCT TAGACAGTGT COCCAGCTTG	420
	AAACATGIGT TACTCAAATG GITGGCAGTA ACCITACATT GCCCAGAATG GGTGATGCGG	480
20	TTAGAAGTOG TATAATCCAA CTOCTTCCAA ACATCAGCGT TATTAGGTGT AAAGAAAGCG	540
	CATCTCTOCC ACAGAATTT AGATGGAGGG CGCAAATTCA GTGCTCTGGA AATCTCATCC	600
25	ATGACAAGTG CAACATCTTT GTATTTGTCC CACAGGATGC CTTTTAATGG TAGGTTAGCT	660
	AAATCITICA TCAAAATTGA AAGTGGTCCA CCTTGTTCTC CATGAGACAA	710
30	(2) INFORMATION FOR SEQ ID NO:812:	
	(i) SEQUENCE CHARACTERISTICS:	
95	(A) LENGTH: 662 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10		
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1517UP	
15		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:812:	
	CATCCTCAAA ACTACAGAGC GAAGTTGAAA AAGATCATAT TITGATAGAG CGTAAGCAGT	60
55	GOGATGAAGC ATACOCTCTT CTCAAAGGTG TTGTGGATAG ACATCCACAT CTATATGATG	120

	CACATTCAGC ATTCGGTTGG TGTCAGCTGC AGTTGGGCGA CACTGAAAGC GCTTTAGAAA	180
5	CATTCCASCT TATTATTAAT AATGIGAAGA GCAGCGACGG CACGICGICT CAGTTCATTA	240
	CCTCAGTACA CTGGCGAACC GCACAAGCAC TTATTACTAA GCAGCAGCAT GAAGATCCTT	300
10	CAGGIAATGA GITTATAAAG ATTOCTITICC AGCATCTOGT ACAATCCCTG AAGATAACCG	360
	ATCTITITGC TCCAGGITAT TCCCITCTIG GACACATTTA CGAAGIGIAT TTTCAACACC	420
15	TGACTCGCGC ATTTAGGTGT TACGTTAAAG CCTTTGAGCT AGATGCCGGC GACCTCGTCG	480
	CIGCIAAATA CATGGIGGAA TACTATAGIG ACCIGIGCAA TIGOCAGGG GCGGGCAACA	540
20	TCTGTGACCG TGTAATCAAG AATGATATGC ATCTCAATTC CGTCAACTGG CCGTACAGAG	600
	TTCTCCCTGT TTATTATTTG GACCTTCAAC ACCACCCTGA ATCCATCCAA TCCTTCCAAT	660
25	cc	662
	(2) INFORMATION FOR SEQ ID NO:813:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 700 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: UNA (genomic)	
40		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1518RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:813:	
5 0	CATCAAATGC CCTTCCCTTT CAACAATTIC ACGIACITTT TCACICTCTT TICAAAGTIC	60
	THITCATCIT TOCATCACIG TACTIGITICG CTATOGGICT CTOCCCAATA THIAGCIPTA	120
55	CATOGAATTT ACCACCCACT TAGAGCTGCA TTCCCCAAACA ACTOGACTCG TCGAAAGAAC	180

	CTTAGATOGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCCTGTTCC	240
5	AAGGAACATA GACAGGGACT AGCAACCAAG GTACTITICTT CAAATTACAA CTCGGACGCC	300
	GAAGGCGCCA GATTICAAAT TIGAGCTTTT GCCGCTTCAC TCGCCGTTAC TAAGGCAATC	360
10	CCOSTIGSIT TOTITICCIC COCTIATICA TATOCITAAG TICAGOOGET AATCCTACCT	420
	CATTICACCT CAAACTITICG CAATACTATT COCCTOCAAG CCCTICTTIC TCCTACCTTC	480
15	TTCAAGCGCC AGCTCCACTC CACGATCTGG TCGAAACCTA ATACGCAGTG TAGAAACTAG	540
	CTCAGAACGC AGTCCGCCCA AGTTCCGCCC ATGGGCAGCA TTTTCAAGTT AACCTTGTCT	600
20	TACGACCGAG TATCACTCAT TACCAAACCC GAGGGITTGA GAAGGAAATG ACGCTCAAAC	660
	AGGCATGCCC CTGGAATACC AGAGGACGCA ATGTGCGTTC	700
25	(2) INFORMATION FOR SEQ ID NO:814:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 706 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1518UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:814:	
	CATCCTCAGA TACCTTAGTC TCTATACAGC GCAAGACATG GCTGATGGCG GCTTTGTTCT	60
50	ATGCAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC ACCTGCCTAA CCTGAACAGT	120
	CTCATCCTOG GCATCTAGCG ATCCCATGGG TGAGCAGCGG AGGATTTGGT GCATTACTAG	180
55	CCAATGGCAA TCCAAACCAA AGAAACCGAC TTGGGGGAAT GCCTCATTGA ATAGCCGGTG	240

	THICGACACT GIGATICICT GAGIGIAACC TOCICTHIGG TIGCCGATAT TAAACCIGHT	300
5	CTGTGAAACA TCGCAGCGGT GTTTAGTGGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT	360
	GOCATGOGGE CAGCTIGITIGC GAAGGTIGTAA AAACCCGAGC TCCGGTTCGC TTIGACACAGA	420
10	AGITACITIC TGIATCICIA TCAGICIATO ACCGAAGGAC COGIGGIGIG CITTOCOCAT	480
	THICCOCHIC TICTHAAGA TAGHTAICIG GINGATCCIG CCAGUAGICA TATOCTIGIC	540
15	TCAAAGATTA AGCCATGCAT GTCTAAGTAT AAGCAATTTA TACAGTGAAA CTGGGAATGG	600
	CICATTAAAT CAGITATOGI TIATTICATA GITOCITTAC TACATOGATA TOTGIOGIAA	660
20	TICTAGAGCT AATACATGCT TAAAATCTCG ACCIPTIGGA AGAGAT	706
	(2) INFORMATION FOR SEQ ID NO:815:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
	(B) TYPE: nucleic acid	
30	(C) SIRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: UNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1519RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:815:	
	•	
45	GATCACACTG AACCCATATA TCABOGAGGT ATGGTACGAT TTGGGCCACTT TGTATCAGAC	60
	ATGCAACAAT CAGCTCAGCG ATGCCCTGGA TGCATATAAA CAAGCTGTTC GCTTAGATCC	120
50	GAATAACGTC CACATAAGGG AGAGACTAGA GGCTTTGACT GCCCAGCTAG CCAACCCAG	180
	GCCCAGCAG CCTCAGCAGC AGCCTCAACA GCAACAGATG CAACAGCCTA GAGGGCCCAGC	240
55	ACCCATTATG TTGCAGCCAA CATTGCAGCA GCAAGACCAA ACAAATCCGT TGAATAACAA	300

360

ACCTROCETTIC TACORRECT CTCCCCACRG AGTTROCETT GCCGGAACAG AGTCCCCACRG

5	CCACACACCA ATGTCAGGAC GOCCTCAGCC GTTGCAGCAG TTGAACAATA ACGGAAGTAT	420
	CCTGGAACCG TCATTGTTGC CGCAAAAGAG GCCTATGGAG GGTGGAATGG ATACATTGGT	480
10	AAATGCCATT TCGCAGCAGG AGTTGCAGCA ACATCAGAAG AAACATATGC CTTCTCAGAA	540
	CCATCCTAGT TTGGCCCTGG CTACAGGACA GCCGCAGCAG TTACCACCCG ATGCCGCTCC	600
15	CATAATACCG CCCGAAAAGA AAGGTGCGCC TCTCCCCCCAG TTTCAGAAAA CTGAACCAGA	660
	OCATOCOOCA AAAAGACTGA AGCCCGAGCA GAATAACGT	699
20	(2) INFORMATION FOR SEQ ID NO:816:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 696 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(2) 101012011. 111000	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI519UP	
35	(A) Chandra. Employe	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:816:	
	GATCAGGIAT COOCCAACAT ATCOCCTICTC TCCATACCGT CCAACATTAT CCTCATACAT	60
45	ATAGACTATG AAGTGACOGA COOCAAGGTG ATCGATGTTA AGCTGGTGCT GGCAAGCAAC	120
	TICCACAAGI TICACIACII CAATOOCCAG GOCAACAICC TOCACOGGIC ACITACCACG	180
50	TATAGOGACC TOCACGAGTT CCACCACAAC CTGAAGTTCT TAACCCTACT CGACGCGTGC	240
	TCAAGCATCG ATATCGAGTC CAATGTGTCG CAATTCGATT TGTTCCAGTA TTACTCGATG	300
5 5	CTCCCCCCACT ACATGCACAC CTACCTGGAC GACAATGGCG CGCACCTCAC GGTGCAGACG	360

	AACCIGAACG ACCGITTIGG GATCIACTIG CIUGACCATT COGAAAAGAA GGTCGCCAAG	420
5	CTGACATTTG CCGCTACGCA GCACCCCAAC CAGCGGTATT ACCAATACAA ATACTCGAGC	480
	GAAACGAAGG AGTIGGATCAA CCAGTICCCCC GAGTICCTATA CGACCGGCAT CACGCTIGGTIG	540
10	TTCGAACTIC TCCGTGACCC TCCGACGTAC CTGCCTAAGG ATAGTTTGCC GCCAGAACAC	600
	CCIGATGAGG GCTTCACGAG TGCTTCTBCG TCCCAGCTGC AGCGCCGCTT TGCATTCAAG	660
15	TGTCAAAATC CACGAGTCAC CCTOGTAAAT GACTTC	696
	(2) INFORMATION FOR SEQ ID NO:817:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1520RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:817:	
40	GATCTTCTGG ACGCTTTCCT TGAGTTCGTT CATCTTGCCA AGCACGTCGA CGTTGGGGTT	60
	GCCCGCAAAA GAGTTGAGCA TCGGCCCAAG GCGGCCTGCA ATGGCGCCAA ACTTGTCTAG	120
45	CACCITCGIG AGCGIAGITG GGAGCIGCAA AAAGCGCAAC GIAIGGCCCG TGGGCCCGGI	180
	GICAAAGATC ACCGIGICGA AGIGCICGCC GICGCCCIGC TOCIGCITCT TGATGIGIFIT	240
50	CATCACCICC ATGAACGAAA GOGCCTOGTC GATGCCCCGA ATGGACCCCG TGAGATCTGC	300
	CACTOCOCCO COCTOTAGCA AGOCOCAÇÃO COCOTOATOA TOGOCOCOCT TOGOCATOCO	360
55	CATGICGITC ACGICCITCA ACGCCGCCGA ACGGICGATT TCCATACACG ACAAGTTGTC	420

	CANOCCOGIG ACCINICOCA CGICCTICOC AAACINCICG TIGAACOCAT OOCTAACGIT	480
5	ATGCGCAGGA TCCGTCGAGA TCAAAAGAAA CTGCTTIAGTG GGCTGCGCAA GCGCCATCTG	540
	CATOSCAATG CACCACGAAG ACGTOGTCTT GCCCACACGG CCCTTCCCCCC CCACGAAAAT	600
10	CCACTIGIGI GITGIAGAGI TGATCAACGA GCGCAAAGAG GCCTCTGGIG TAATATCAGI	660
	CATGGITGGT GTACCGCGTG AATCTGAGAG TGCAGGCGAT CTGAGATCTT	710
15	(2) INFORMATION FOR SEQ ID NO:818:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 685 base pairs	
20	(B) TYPE: mucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1520UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:818:	
	GATCAAACAG TAATGACTIT GITAACGGIT TIGAAGTACT GCACGAGCTG CGACTCCTCA	60
40	CIGCCCIGIG GCGCCACAAG CGCCCAAATC ACAGCAACIT CGCTTICAAA CTGAATGGCC	120
	TOCTOCATOT TOCOTOCCAA COCAACTIACO ACCACCOCTOT COCCAGOCTG GCACACCTICO	180
45	TICAGATAGO GOCCCATOAA COCCAACCAGO GCACCOTTIGO GCAGGIGOGO CGAGTIAGTICA	240
	TOSCCATOCA CACCATOCAA CTOCTCTAAT ASCCCTOGT ATTTGTOGTG CTOCTCCGTG	300
50	COGAACCOCT CCACCOCCTG CTGCACCOCT ACGGCGCGCGC CCCCCGCTTGC CCCCCCACTC	360
	TTCTCTACOG GCACATCGGC AAGCACCGCC AGCACCTCCA GCTCATCTGG CTTGAACACC	420
55	GICACCCGCC GCCICAGGCC GGAGCGGACC TICICGAACT CCGCTICGCT GAACTCIGTC	480

	TOCOSCITOC TOCOSTCAAT CCACITOCC COCTGCACCA AGATGAGCGT CCTGACCACC	540
5	GCAACGCCAA CCATCTTCCA CGCGCTAGGT AGATCTTCCG AACCAGGGCC CTTGCTGGCG	600
	TATIGOCCOCA AAAGTOCCTG CTGACGCCGC AGAAGGAACA ATCTAGGCTT ACAAGTCTGC	660
10	GAAACATTIG TOOTGOGAGT TAGOO	685
	(2) INFORMATION FOR SEQ ID NO:819:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1521RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:819:	
35	GATCGAATCT KGTCTGAGGG TCTTCCACGA WITGCAATGC AATCTCCGGA TATCCCGCCT	60
33	TCTGTAGATA CGAGATGATG TICTGOCCCA CAAGGTTGGA CGTACGAATG AGACGCAAGA	120
40	CTTCACCEAA GITCTTGTTC ACCAAACCTT TCTTAAAGCG GTACTCCGTT GGGTCAATGG	180
	TCANTATCTC ANTATCOCCS TCTCTGTTCA ANGCATATAT ATGCTTGCCA TGAGCTTTGG	240
45	TAATGTATAG GGTCTTGCTC AAAGTTTTTA TGATCCCGCT GTCACCATTC AATAGGCAGT	300
	ACTIVAATATG GITCAAAGTA GACAAGAGCA GAACACCAGT TTCATCOCCAC GCCCCTGACT	360
50	TGATCCTGAT CGTCTCATGG TTAGACGIAG TAATCTCCAA CTTCCTAGTA GCAATGGTCA	420
	GOGIGIGITT ACTOATIAAA GCAACGTATT GCCCATCIGG GGACCAGACT GCATATTIAA	480
55	CONTRITORS ACCURACING GOGRAPHITH TOCCONGRIG CARGIOGRAE ARGACIACOS	540

	CCTTTGGTTT CAAGATGAGT ACCOCACCAG GGCCTCCATA GACAATGTCT TTAACAGTTC	600
5	CTICTATCTT GATOGATTIG GITACCITGT TGTCCAACCC ACGIACTTCA AGAGATTCCG	660
	ACCCAGAGIT GUAGACAGOG TUACCUATOC OGAGOGACAA AAGUCGCAAA GCUTCCCUUA	720
10	TC	722
	(2) INFORMATION FOR SEQ ID NO:820:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 577 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1521UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:820:	
	(ALL) SUSPENDED DE LA CONTRACTOR DE LA C	
35	CATOCACTIC CCACATTACA TGATAACATC GAAGCOGAAG GTCGCAAGGG AAATGTTGCA	60
	CCAGTATCAC TITTATWCATA GOOCCITCAT CAGCGTACAC GOCAAATCAG AAAGCCTCAT	120
40	CTTGGGCATG CCCAAGAAGA CCACCGGCAG TTTGATCAGC TCATCGAAAG TTTTCCTATA	180
	TOOCAGAGCA GOOGTCACCA TGAAGACAAG CAGAGGCCCA GOOGTCATCA CCOCAATTGT	240
45	ATTICATISTICA TICTIACICIAGE ACCACATACA CTACCAGTIC GIGGOGAGOG ACCTOCATAC	300
	TGTCCAGACG AACTACTACT ACCAGGGCCA GCTCAACCAC TOGAGAATGC GCCGCCATTC	360
50	CCTACCCTICC AACACCCACG ACCACTACCA CATATACCAG GITGACTGGG ATGCCGAACG	420
	CATOCACTOG ATGGTCGAGG GOGAGATAGT GCGCACCTTG TTCAAGCGGG ACACCTGGGA	480
55	CCCGGTCCAC AAAATATACA AGTATCCACA AACGCCCATG ATGCTCCAGA TTTCCCTCTG	540

	OCCCOCOGGIC ACCCCCGATG COCCOCAGGG CACCATC	577
5	(2) INFORMATION FOR SEQ ID NO: 821:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1522RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:821:	
	GATCAAAAGC GAACAGCGCA CTTATGTCCT GCCCAACCGA CGCGTGCTCC TCAATACCCA	60
30	ACCACCACTC CCTGGCCTGC TATCTGCGCG TATTCTGTCA GAACGATCGC CGCTAGAAAG	120
	TTACCAAGCE CETCACACCT GTATTCCCTG GCTTCTCTCT CGGCCTTCGA TGTGCTCGCCA	180
35	AGTAGITETE CACGITETOC AGCTGCCACT GGAAACGTGC AAACCAAAAC AAACCTGACA	240
	CCACTICIGI CICICGAIGG GGICCAGCCI CCAGAACTCC CAGGGCACAG ATTITGACTA	300
40	TAGCAACCOC COCCACTAGC ACTCAAGAAC TITCAATTTT COCTTGAGCC CCACCTTGTT	360
	TTTCGAAGAT TCTGACCTAT CCTCCTATCG ACGTCAGGGA CACAAATCAC ACTATAGTAC	420
45	CTCGAACAAC AGTACAGAAA AGAAAAACCAG CTGCTCCAGC CAAAATTCAC AAGTCCCGTT	480
	ACCIGCTAAG GCCAATTOGT GATACTCAGT CITTAATCIT TACCCAATTG GGAAACTICA	540
50	CCAAGGAGAG TCTTGCGTCT TAAGGTTTGG CAGTTTGGTT TAAAAATTTT CTTGCACGAA	600
	ATGICAGAAT GICTOGGITC CCCTTGICGG TCACGTGGGT GICGGTCACG TGGGTGCTAA	660
55	TCACGIGACA CGIOGATGAC GACTGAGGGG GAAAATTITGC AGGTT	705

	(2) INFORMATION FOR SEQ ID NO: 822:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 718 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1522UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:822:	
25	GATOGACAAT ATTOCOCCAC CAGGOGCAAG AATOGAGTGC ACACAGGOCA CGCGCGCATO	60
20	COCCUTOGRA TOCCOCCCC TOCCOTOCAG TOCCCCCCG GCCCCCAAG CACACTACCA	120
30	CAGTIGUCUG TOGUGOGOG GOCAGOCCAC GCCGCGCAGC TGCGGGCCTGC ATTCCAGCCA	180
	COCATOCACE AAGAGCCGGG TCACACTGCC ACCCCTGGCG TCGCTGCTGC AGTCCAGCGG	240
35	CTACATGGGG TICAACAACG AGCCGCGGGC CGTCACGCGC TCGTGTCTAG GGCCCACACA	300
	TCCCGAAGGC CATTACGGCA GGGACATGCT GAGCAGGGCG GTGGGGCACG CCCCGTGTTA	360
40	CETERBOORC CACACCOCT TOCTACCOCT GROCEACOCC ATTROCOCCOC COCTCOCACC	420
	CAAGCCATCG CATCCCTGCG TCGCCGGGAA CGCGCAGCTG CCCCCAGCTGCCCCAT	480
45	CGTGGGGCCC GCGGCGTCCC ACGCTACGAA ACGAACAAGA CATGCCTCGT TTGTGGCAGA	540
	CGATGTACCC GICCCAGCAC GCTCAAGAAC ACATGCTCAT CCACACGGGC GAACTGCTTT	600
50	TCAGTOCAGT TGGCCCGGGT GCTCCCAAGCG GTTCAACGTC AGGAGCAATA TGAACCGACA	660

1081

718

TOTOSANCTOC CACAAGOGOC COCTGATGAA GGAAAGCAAG AAGAAATOCA GTTCTCCC

(2) INFORMATION FOR SEQ ID NO:823:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
5	(B) TYPE: nucleic acid	
J	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1523RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:823:	
	GATCTIATCT AAACCGCICC GCGATGATGC TITGGIAGCA ACGGAAGCCC GCATTTCAAA	60
25	GICAACATCA GCGGAAGCTT GGATAGATGA GAAAATCACA GGIGTCACAT GGCGCGAGAG	120
	CTGAATTOGA TTCACCOCTT TOCTATCAGT GGGIWAGAGG CGTTCACTGG GCTGTTCTGA	180
30	ATTIGAACIT CIGGAGCTAT WCGAGGGGTT ATGAGCAAGT CCAAGTTCCC GCGTGAAAAG	240
	CTGATCCTGG TAATACTCGG TGTAATCCAC GCTTTTCTGC CAGCAAAAAG CTGGCGAGTT	300
35	TOGANICITT CCTTTATCOC CCACGICCOT GOGIACATOC CGTTCAATOC TATTTOCTCA	360
	TGTAACTGTG GGCAGAAGTC GTAGGCAATG TCTAGATAAG GTTGACGCTG AAAAGCTATT	420
40	ACGITICCAAT AGCIGOGGIT CACAATOGTIC TACTITOGGCA CAGCAACCTIC CTGOGCTGCA	480
	TOTOGGIGAG CIATTAAAAA TOTOGGCCAC CGAATAGAAG AGCATOTTIG GGIGAGCGCG	540
4 5	ATTICAGITICC ATGAGATCAA CAAAGGATAA AATCCOGAGG TTATCAAGGG AGAATTITGIT	600
	ATCATACAAG AGCCAATCAT CACTGCAGIT GGCTATATIT GGATTATIGI GATATIGCCT	660
50	CACAGCAGIG TITATCCOGT CITTITOGCA GICATATACC ACAATGGATT GT	712
	(2) INFORMATION FOR SEQ ID NO:824:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 649 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
3	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
0	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1523UP	
15		
, .		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:824:	
20	CATOGACAGA ATGAGCAGAG CCATTCTGAG AAAGCAAACA CCCCCCATTG CCCTTCTGCG	60
	ATCCCTGCCA CAGAGCGAAA TGGGCCCAGA AGGTTTGTAC TCGCCGATCA AGGATCATCT	120
25	GCCCTTAGCG CCATCCCACC TAGTAAAAGG ATGCCATGGA TGCTGGTCGG AAATGCCGTG	180
	CGACTICOCOC AAGACATIGGA TITTTATICAAC ACCAGCTICCA AGATATTICGT COCAACACAC	240
30	ACTICOCACA CGAATIGOGC AATGAACATG GGTCAGAACA GTACATTATC CCATTCTCTG	300
	ATGAACOCAA ATATTATAGG CTCAGAGTCA AGCACOGCCA TTAGCAATCC ACCTATGCCA	360
<i>35</i>	TOTGAAACTG AGGAACGITA CAAAAGTGIT TTACAGAGAC TOGGTAAGCA TGTOOCTOGG	420
	GETAGAGGCC TATCTCAGCT TTATAATGAG TTTTTTGGAGG ACGAGCGCAT CCTCTACGGC	480
40		
	TIAGGIOGIG GAAGIGAATA TGITGAAGCA TACTOOGATA GITTGGATCA AACAAAAAAC	540
	AATGTGAGCA TOGAGACTOC GTATGAATCT TCTTTGCTAG AGCGCGGGGG CCAGCAGGTT	600
45	TTTCTGTCTT TCGCCCCAACG CCCGAAGATA GAGCTACTGA GGATCATGT	649
	(2) INFORMATION FOR SEQ ID NO:825:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 660 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1524RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:825:	
15	CATCHTHICA AACAACHGAA THICHGGAAA TCGAAGHGCG GHGACHTGGA CAAAAHTAAG	60
	CAGGACITAC TGGCCAACAT GGCGACGAAA GAGACGGACT TCAACAATGG ATGCACGGAC	120
20	TATGAACGTA ATATAGTTGA ACTTCAGCGT CAACTATCAG AAAAGTGCGA CGCTACAAAC	180
	GAACGCTCTG TCACTTCAAC CTCTGCCGAT GTACCTGGAG AAACCAAAGA ATATATTGAG	240
25	TOTOTOAAGG AAGTOAACCG TAGACTGGAA GAACATATGT TIGCTGTTTT TGCCGGGAAC	300
	ATAGIGTIAC TOGAGAACAT COOCCTOCTT CTTTCIAGAG OCCCTGACAA CAAGITACAG	360
30	ATTATACGCG TTAAAGGTTT AAGGAAAAAC ATAGATGATA GTATAATAAA GCACAGCAGC	420
	CCTGTAATAA ATTCACATAT GGTGAAGAGC ACAGTTTTCC AGGATGTGAA GAACTTATTT	480
3 5	GACGACCTTC AACTGACCCA ACCTGTTAAC GACCAACTOC ATTTTGTTAG TCACCTGGAA	540
	COCTITIATE ANGAGGATET ATTICCAACT TOOGTGATCA AGAGGITCAC CCATGIAGAG	600
40	AACCTGGCTA MGAGCTCAGA AAGGAAAATA AGGCTAAAAA AAGCGTATTG AAAGACACCA	660
4 5	(2) INFORMATION FOR SEQ ID NO:826:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 671 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	· · · · · · · · · · · · · · · · · · ·	

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: PAG1524UP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:826:	
10	GATCTATCCA AAGIGIGAAG CTCCTAGACA AGITCGTCCA TCCCAAAACC GGGAGAACCT	60
	CITITOTOCIA COGIATOAAC TACCAGIOCA TOCACAGGAC TOTTACCAAT GOOGAGGICA	120
15	ATGTCTTACA AGAGCAGGTC AGTCGGGAAC TAGTCAGGCT TTACAACGTT CAATTCAGAT	180
	AGCCCAATCA GCCCGAGACT AATAAACTTG TATATACAGC TITTGCCGCACA TCGCACCCAT	240
20	GTAACGIMTA GTATGATATC TOCTTACTCA TATCOCACCT GAATGCTAGC AGACTTGGAG	300
	AAATGCCTTA ATACGCAGCA TATCCGATAA CTAGTGCCTA AAGCCAAGTT CTTGGATCTT	360
25	CACAGCTAAC OCTITITICIT TOCTCCTGAT COCAGCTACA AGAATACCAA TCCTTTATGG	420
	ATCTGAAACC GGIACTGCAC AGGATTTCGC TAATATACTG TCCCACCAAC TACGTCGTTT	480
30	TCATTACAAG CATACOGTGT OCTCTATTOG AGAATATAGT OCCCAGAATA TOCTCOCATG	540
	TCAGIACCTA THIGICATHT GCTCCACCAC CGGGCAGGET GCGCTGCCGC AAAATGCGCG	600
35	OCASTOTOGS CAGOGCAAAG TOGAAGGTAC ACCATGGAGT GTOCTCAAAA GAAGCTCTCT	660
	CCCACCAACT C	671
40	(2) INFORMATION FOR SEQ ID NO:827:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 712 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: INA (genomic)	
	(NG) ORIGINAL SOLDER.	

(A) ORGANISM: PAG1525RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:827:	
5	CATCHTCTCT COCTOCAACT CGICATOCGT CCAAAATTIT AACHTAACAA TITHTCACCT	60
	TGACCTOGOC AAGCATCTAT ATCACGTGAT TOCATCTGAC CAACCTCATC CCAAATGCAG	120
10	GCCATTGGCT GCTGCATTAA COGTCTCAGT GCCCGGCTAG AGAACTAGCG TTACGCTTTG	180
	GGETTTACTA GCAAGTGGCC GTGCCGTGGG ATTCGCAATG TGGGCGCGCA CCTTATCCAC	240
15	GOGACACAGA AGIGOGIATT TICOCTIGIT TACATAGATG TOCAAAAACA GIACOCOCAA	300
	AGCACCAAGC AAGCITCAGC AAGACTICAGG GAGGIGITAG AGGCGATAAT CCAATCTGTG	360
ي ن	CTGAATGGAG CAGGCGACGG GACCAAAGTG GATATTTGCA GOCCAAAGTG AGACCATGGC	420
95	ACCOCAACAG GOCAATGCAG TAAACOOGGA CCTGGACGGC GOCATGCAGA AGACGTTCAA	480
25	COCCETCAAC CCCCTGCACT TCAACGTGAA TTTGCCCGGGGCA AGCCGGGGCT	540
30	CUCCUGAGACC CTGAACTOCC CCCCCCCCCCCCC GCAAAAGCTC AGGGTCCGGAG GAGGAGACAC	600
	ATACCGAACC CACCOCCACC TOCACCCCCC CCCCCCACAC TCTACTICTCC	660
25	AGCCCCCCAA GETGEACCE TOCTTCACCC CTTCCCCCCT GAACTCGTCG CC	712
	(2) INFORMATION FOR SEQ ID NO: 828:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 703 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1525UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:828:	
5	CATCATCOCC ATTITCOCIC COCITICATCA CAAAGGCCCT CACTTATACA TOCTTGAACC	60
	AAGTIGGCOCT TACTIGGGGTT ATAGAGGAGC CGCTIGCCGGA AAGGGCAGAC MAGCCGCTTAA	120
10	AGCOGAGCTIG GAGAAACTGA TTGGGAACGA TAAGTCAGAG CTGTCAGCTA GGGATGCAGT	180
	GAAAGAAGCG GCTCGGATCA TCTACGTGGC CCATGAGGAT AATAAGGAGA AAGAATTCGA	240
15	AATTGAGCTG AGCTGGTGCT CCGCTTCGGA GACGGATGGC TTGCACAAGG AGGTACCAAA	300
	ACAGCTATIT GATGCAGOGA TIGAGTITIOC GAAGAAGGAG ACCOGTICAGG AGAGTGATGA	360
20	TCATTCAAGC GATGACAAGG CATCTGGAGG TGAAGAGTOC TCAACAAAGA AGGATGCTGA	420
	CGGIGATGIC CAGCITICAT GATAACAGCC CGGCATTATG TGGAGGITCA TITICATGACA	480
25	ATTGACGGAT GITACTAAGT GTATATTAAG TTAATCCACC TATATAAATT AATAACATGC	540
	AAAGCAATTT AGAATTTGTC GGAAAGCAGG TTAAAGCATG TCTACTCTCC TTAATCTTTC	600
30	GCCAAGCIGT ACATITICIT CICAAGIGAA CGAATICIAT CCACCGGCIG CGICIGAITIC	660
	TAATTTCCTA CGITCGCGTT CTGTGTACCA TTTCCGCGTC AGC	703
35	(2) INFORMATION FOR SEQ ID NO:829:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 725 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
45		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) CRGANISM: PAG1526RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:829:

	GAICIGGCCG GGACCITIGAG AGGCGTCTGT ACCITICITIC AGCACAACTA TIGTGGCAGC	60
5	TIGGITICCA AAGTICATCC TGAGCTCGGT GGTCGTTCAG ATATGGTGGG TGATGGCCTC	120
	GTCACGGTCT GTCAGCTTCC TGTACCGACG ATGACGGCAG TTTTTGCCAC TAGGCCATTT	180
10	TTTTTTCAG CTCTAAGATG GCAGACGGCA AGGAGAATGC TCCAGGACAC CGGATAGAGC	240
	TOCAMICTON GOMAMACATO GOCTACTOCO CONTROCTOC TOCTOCATAM CACTITOTATO	300
15	GCTTAGTTIG TGCACGTGGT CGGCGCTTCA CATTGTATCT CGTGAATTGC GTACCGGTAC	360
	TATATTACOG TIGIGIGOCC GAGCOGICIA ACOCOCCIGA TICAAGIGIA TOCTTACAGC	420
20	TGTTCACAGO TGAACACTCA GGTATOGTAA GATOCAGGAG TTOGAATCTC CTCGCAACCA	480
	ATATTTTTCC CCCCGTTTTT CCCCCCCCCCCCCCCACACTCA TTTCCGTCCTA	540
25	CCGITGGAGG TAAACTGTTG GAATCCGACA GTGGGGTACC GAAACCATCC CAGCCTCTTA	600
	TTACTAAGCT GGATCGTGCA CTGCAAGCGG TGATATTGGA ATCGTCCCCCA CGTATTATTA	660
30	CTAAGCCGCC ATCTTGCCGG CCATGAGGAG GGTACCGAAA ACCAATCCCC AATTTGCATT	720
	ACTAA	725
35	(2) INFORMATION FOR SEQ ID NO:830:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 701 base pairs	
40	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1526UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:830:

	GATCGICACC AGGICCCCGG TCTTCGGGAA CGTCTTGCCA TCGCCTGGCG ACAGICTGTC	60
5	GATCTTCACG TTACCTTCGA TTACCTCCGA CATGCTCGTT GCTGCTCCCG TGGCTCCCG	120
	AGAGTGATCA AGTIQCGTGTT ATTAAGGCCC CCAACGCCAC CCGCCTGGCC GGGTAACACG	180
10	TOCOCCOORDE CTOCOCCOCOE TOCOCCOCTOTO COCCOCATOCA COCOCATOCA	240
	GEOGRAFIACA COGOGIIGOGO GCACTITIGOG COCCOCCAGOG COCCACTIGO COCAAACCGGT	300
15	AAACTTAGTA CGCAACCGCC CAGGGGCCCGT CATAGCATAC GGAGGCCAGA CGGGGTAAGG	360
	CCGIAGCCCA GTCCCCAAIG CCCCCACGAT ACCTCTTIAG CCACGATACT ATTITAAGCC	420
20	GIACAGOGO GCAGOCCATO GTGCAGOCTG CAGTAGCAAG CTGAGACAGG CTGGGCAAGT	480
	CTACACCTOG GACACACCCC GCAACCTACA GGCCGCGGTG GCCGCGACGC GTCACACATT	540
25	TICOGTOCCA COCCOCTOS CACCACCACA AACACCOCOS ACACAACCAA ATGCMCAACT	600
	AAACCCCCCC GAACCCCCACC CCATTTCTTT TTGCCCTTCT GTGCGACGTG GAAATTGTAT	660
30	AAATAATGOG AGCGGCGCT GGTCTTGCCC CCTCACACTC T	701
	(2) INFORMATION FOR SEQ ID NO:831:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 705 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1527RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:831:	
££	GATICUTOCOTO CULATOCAGAA ATGGGGAACTUL CUUTAGACAAC GGGGAATUAA GCCCCTUTUTC	60

	CAMPACTURE ACADECAGE ACADECAGE ACADECCOC COASTASTST	120
5	CIGITCATGI TOCCICATGA ANGGIGICIC TATCAAATCI AGCTOCATCA TOGCAGAGIA	180
	GITATTATCT TICTICCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGGA TTACAGTAAA	240
10	ATAATGGTAG AACGGGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGGCCGGTA	300
	GAAGATOGIG OGGCCCTGCT TCTCTATCAC AAGATGGAAAC TGCGAAAGTC TGTTCACGGG	360
15	GCACACCGIG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
	CCCCCCCACC TCAGTCTCAA CCTCGTCGAT CCGTCGCACC ACCTCCACAT TCCCCCTCGA	480
20	GCTGAACAGC TCCCGTGAGT TCACGTCGTG CGTAAACTCA GACAGGTACA CACACTCGGG	540
	CAGGCCCTTC CCAATACATG TATAGCACTT CGGCCGCGCC TIGTIGCACT TGACGCCCCG	600
25	CTTCCCCCAG AACACCCCAG ACTTCCCCACC CTTCCCCCCTG GTTTTCACAA TCTTCCCCATC	660
	GGACTICTIGCC ATCCCGCCAG CTTICAAGCAA AATGATTAGG CTATA	705
30	(2) INFORMATION FOR SEQ ID NO:832:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(si) OPICIARI OCERCA	
15	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1527UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:832:	
	CATCOCCEAC GTGGACCACT GCCCCCACAT GCCCCCGCCC ATCCTGGTGG TTTCTGCCGA	60
55	CCGCAAGCAC ACGCCATCGA CGAGGGGTAT GCAGCAGAGG GTGCACAGGT CGGACCTCTT	120

	CAAGGAGGC GTCGCGACGG TGGTGCCGCG GCGGTACGGA AAGATGGCGG CGGCGATCCG	180
5	OSOSOGGAC TIOOCGACGI TIOOCGCCCT GACGATGCAG GACTCGAACT CGITTCACGC	240
	CACCIGOCIG GACICATITO OGCOGATOTI CIACATGAAC GACACTICOC OCCOGATIGI	300
10	CAACCTGTGT CATCTGATCA ACCAGTTGTA CAACCAGACC ATCGTGGGGT ACACGTTTGA	360
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	420
15	CCTCTCTCCC GTCTTTCCCC CCAACCACCC CTCCCACCACC ACCTTCTCCA CCCACCACCC	480
90	COCCACCTTC COCCCCCACT TOGACCACTG COTOCCCCCC AACCTTCCCA CCCACCTCCA	540
20	CCACCACTTC CACACACCAC TTGCCCCCCT CATCTTCACC AAACGTCCGC CCAACGCCCC	600
25	AGGACACTAA ATOCTOGCTC ATOGACOCOG AGACGOOCCT GCCCCCTGAC GCTATTCTCC	660
	TGCTATTITC TGCTCTGTAT ACCCTGCCAG AACGCGCTAT ATATATAGAA TATGCATT	718
30	(2) INFORMATION FOR SEQ ID NO:833:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 701 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEDNESS: single	
	(D) TOPCLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1528RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:833:	
50	GATCACTGTA TOGAATTTGA CACOCAAGGA AGOCAAAACA TOGTGGGGGG ATCCCGACAA	60
	TOTOGRACAT ATGATATOOC TTTCTOCRAG GATGOGTGCC TGAGCTTCC TCTTATTCAR	120
55	TICTCTATIT CTATAATICA COSCATICCT TICCCTCASC TCATCGCGCT GCTTACCTAG	180

	CICALTAAIC TICTIGCICA AGICCCICAA CITTAGCIGI AICITAGATA TCTCATCAGT	240
5	TGAGAGITTA CTAGICUSCU AACCATOCTC TTTATTCATC ATATCCCTGA GCTTTCTCCT	300
	CTCCCCTACG CCGICATGAA AACTCTGATC TAAGTTCCCA TCGTGATTTA TTTCGTACCA	360
10	CTCATTCAAA GCTCGCTTGT CAACCAGCTC TTCCAACGTT AGGTCTCTGA TAGCAGCGTT	420
	AACTOCATCT GATTTACCAA TOOGCACTAA TTTTGGTTTG AACAACTTGC CGTCAGTATC	480
15	GACCAAACCT TCTCTCAGAC GCAACACAAG CTGGTCAACG GCTGCATTAC TGGGTGCACA	540
	TATCAGAACT THTTGTTTCT GTAGTAACAT CTCAGTAGAG GTAGCGFTCG ATTCTGTCGG	600
20	ATTICICATA ACATTIGATG GTAGTGCTTT TGCGGTAGTT AGGAAAAACC CGACGACACC	660
	AAGAATAGTC TTAGTCTTAC CAGTACCAGG GGGTCCCTGG A	701
25	(2) INFORMATION FOR SEQ ID NO:834:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 711 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1528UP	
70		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:834:	
	GATCCAGCAT TTCGCCGTAA ATCGGCGTAT TCCGCACGCG AAGGTGGGAA GCTTCAACGA	60
50	GITGATCIOC ATGTGGCGGG CGCAGATGGT TCTTCCACTG CTGCGAGACT TTGATGCCTG	120
	CAAAGTATCA GATGCTGTTA TTCTGGCGAT GTATGAGATA CTGCTGAATC CGCAGATGCT	180
<i>55</i>	CCCGTCCTCG CCCGAACTCA AGTACTACTA TGATCTAGCA TTCAACCCCA TGTATCAGAC	240

	GOOMENIGHS CITTINGACE NEWSWANDA MENAEGINIE MAIETOCICE INCETCONST	300
5	OSTATATICA CAGATISTACIS SCTISCOCTISA ACAGAGITICT TISSICAACAC GTICTICTTISCIS	360
	GCACTTCTTC GAGAACGAAT ACTCAATCAC AAATGAAAAC GTGACAACCG AACTGCTTGA	420
10	CGAAATCACC TATCATTTTA TICAGTTACA GITGAGCAGG ACCAACAGCT CGTATTTGAG	480
	CATGATTOGA CTATTCTOGA GCAAGATGTG CCCGTTCTTT GCGCTGATGC ATGTTGATGT	540
15	CITAAAGGAG TACTITATIG AGCICAAGAA TATTAAGICA TIGOGGICCA CGACTAAIGI	600
	TCATATIGAA TCIGITTICA AGGIATITIA TCACCATCIC ATAATOCAGG TAAGATCAAA	660
20	ACCGITICGAT ATTICTICCICC GTATTITIGAA ATTIATICCTCC AAAAACTACG G	711
	(2) INFORMATION FOR SEQ ID NO:835:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1529RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:835:	
45	GATCAAAAAG AAGGCGATTG CTATGGCGAC GGTGACTGCT GCTACGCCGG TCTACGCTCT	60
	ATATOCTICC TCTCCCATGT TGGTTGACAG CTCCCCGTTG ATCAAGCTAG AAGGCACCAT	120
5 0	TICTCTCAGT AGCAAAGGIG CTACTAATGA TACTGATGTT TICATATTAC CAGAAAAACA	18
	TICIGCIGIT COGGCTACA ACACAATCAT TOGITTCCTC GTACCOGCCA TGAATGCCTT	240
55	CAGGCTTTAT GGCAGGCCGA AAACACTATC GGCGAGCAAG GATGACACAA ACTCACTOCT	30

	GITTAGICTA OCAGOGOTIC CACATGIGCA CTACTIGCIG GICTAGGATT IGCTICCATT	360
5	AGTGAATTCA GCCTCTGGCT CATGGACGAC GCAGCAGTGG CGCAGACAAA TCAAGGCTCT	420
	ATTACAACOG AGGETAGCOG CTGOCTATCA GGGATGTGGT TCAAGCTCCG GTCTATCCCG	480
10	COCTOTOCO TOCCOTOCTO TOCOCTOCAT GAGIOCIACT TOTTTGTCAT COCCOCATTT	540
	TOCTOCOTICC ATTOCCTTTT COCCTACTGA GTCCAACTAC ACTITITATGT CAAGTCACTC	600
15	AAGAATAACT TCACTACATG ATAATATOCA GAGACCATAT TGAATACOGT GOCCAGCACA	660
	TCCGATAATA CWCTGCACCC AAACAATATG CTATCTCCCG CAGGTCTTGC CCCTGATGCA	720
2 0	TT	722
	(2) INFORMATION FOR SEQ ID NO:836:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 691 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1529UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:836:	
45	GATCCCCCTC AATGCCAAGT AGAATGTTTC TCGGGGGGAGC CCATACAGTA CCGCCTCCTC	60
	CTCATCCCCC CTCTCCTCCT CCACGTCCTC TCGTGCAACA TCTAGCAGTT TCCCCATAAC	120
50	ACTESSEATE GICATISCICA COSCITOCOGA TATCACGATC AGCACCAAGE COCATACTAG	180
	AGACTIGAGO TOAGOCCOCO COAATIGGAA CAGTOTACOO ACATOCTIGG CACCIGATGO	240
55	GITGCCCGTC GCCGTCCACA GCTCCACTCT TTCTTGCTGC GGTTTCTCTT COGTACTTGC	300

	COCAGGETT GETETTEAGT TTAGECTEGT TTEAATTETT GECCATGOOC TGAACGAAAA	360
5	COGGETGOOT TGATGTAGAT GATTGAACGG CGCCCATCGC TGCATCCCCAA TAACAGGCCT	420
	COSCACCIOC TTAACACCTA GOGATAGOCA CATATATGIT CTOCTOGAGG TCATATICCC	480
10	ASTITUCITO TAACCTCACO ASCOTTIGIAS GOCTOTOGAS TICOCTIGIAA GIGGIGAATT	540
	TOCOCATOGG ACICATTITI CATOGAGAAT AAATAATTGT ATTACAAAAT AGAGATOCAT	600
15	COCCASCIAG TOGACCCAG CITACIATACA COTOCIGGAG CITITOCAGIT CITACOSCACO	660
	GGITTTCGGC TCCATGIGAC TACAACAITT T	691
20	(2) INFORMATION FOR SEQ ID NO:837:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 714 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPCLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGL53ORP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:837:	
40	GATCCCTCTG CTACAAACAC ATACCTAGAT TTCTCATATT TTATACTGAA TACATATAAT	60
45	ATATCATTIA ACTGICTICA TICATGAGAC GIOGICIAAG TICIGIOCIG CICAACTIGI	120
	TITICCACIT GICAGOCTOT TOGOCCOCCA GTACGITICAC CACATGOACG GCTAGOTICC	180
50	TCATTCCTTT GCTCTCACGC GTATCGTTGA TIGTCTGGGC ACCGGCCACA GTTTCCTCAC	240
	TCACTACCAG GOCTTOGATA CCAGGITOGC TACCOGTGGG CCCGCACAGG TCATGIAACG	300
55	CAAATATTTT GATTTCCAGC CCCGGTTTCA GCCTGTGAAG GAAGCTGCAC ACGTTATGGC	360

	ATCOPTICATE GAAGGACTCA ACCIDENCE TOTATTICTT GITCOGCAGE ACTICITICAT	420
5	CTGTAATCCC CACGATCAGC CGGGACGCAG TCACGAGCGC GGCAACACTG AGCAATAITT	480
	TATETICCETC GIGTAAGTGG TCGAAAGTGC CTCCCAQCCC GCTAACAGCG TACTTGTCTC	540
10	TACCOCCACT CTCGACCOGG CCCGCAGCOG CCATCGCCGG ACTATCAAAC AGCTCTATCT	600
	GCCTGTGCGG GAACGCATCC TGCAGCAGGC GATCGCTCAG GAATACAACG TCCCACTTCA	660
15	TTCGGCTGTA CGCTTCCATA CTGACGTTGA ACAAAACATT TATCGGGGTC GTGT	714
	(2) INFORMATION FOR SEQ ID NO:838:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(b) forobodi: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI530UP	
	(V) CWRIATON: EWITOROPE	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:838:	
40	CATCCTOGGA CGACATCGAC ACCATTICTA TCGGTAACGA ACTTGTGAAC AACGGCCAGG	60
	CCACCETGEA CCACATGECT GETTACATCA AAACTGGCCG CAAGTGCCTC GCTGAGGCCG	120
45	SCTACAAGGG CCCAGTIGIT TCCGIGGACA CTTTCATCOC TGTAATCAAC AACCCTGGTC	180
	TATGIGACCT ATCAGACTAC ATGGCTGTCA ACGCCCACCC ATACTTCGAC TTCCACACTT	240
50	CTOCTOCTAT GOCCOOCCCT TOGGTTTTGC ACCAGATCCA GAGAGTCTGG AGCOCCTOCA	300
	ACGGTAACAA GAAAGTTGTC ATCACCGAGA CCGGCTGGCC TACTCAGGGT CAGACTTACG	360
55	GCAAGGCCAT TCCATCCAAA GCCAACCAGA AGATGGCCTT GCAATCTATC AAGGCCACTT	420

	GIGGIGATAG COCTATOCTA TITACIOCIT TOGACGACTA CTOGAAGCCA GATGOGOCTT	480
5	ACOGICTOGA GAAGTICTOG OGTATOCTAT AAGTTOCOGT GTOCTTCTTT ATGACCTGTC	540
	TOTITATITT GOTOGGAACO OTTACATOCA CATOGOGGGT GOOGGTOCAT GOGCCTOCAG	600
10	CCTCCCCCCC TOCAACTTTC TACATCCCCC TACTTTACCT CCCACCCCAC TTTTCAATTT	660
	CTTTGGCACG TGGTACTGCT GOCATCCTTC TCATAGAACA CAGTGTGCCC ACAGGG	716
15	(2) INFORMATION FOR SEQ ID NO:839:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 723 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1531RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:839:	
	GATCTOCATC CTCGTGATOG AAAATACOOC CATGCAGCTA ATTTTGGAAT GGTTTCTGCA	60
40	TACOGIAAGA GAGATGECIC CAAATCATAC CCAGITACIA TOCTTGTGAC TAACTITTCA	120
	AMOCCGACAC CTACCAGACC TOCTCTTCTG AAGTTOGGAG AACTCACAAC GITCTTTCAT	180
45	GAGTTAGGCC ACGGCATACA CGATTTGGTG GGTTCCAATG ACTTGGAGTC GCTCAACGGG	240
	CCTGGGTCTG TCCCATGGGA TTTCGTCGAG GCGCCCTCTC AGATGCTGGA ATACTGGACG	300
50	OCACOCCTIC ACETITITAAC TATGITATICC AAGCACTACG AGACAGETIGA GAAAATCCCG	360
	AAGTOGOTIGO TOGATIGOCTIG GTTTTAGTIGTT GGCGGGCTICA ATTICAGGATT GGCCAACTTIG	420
55	GGCCAACTGA AACTTGGCTT GTTCGACATG TATGTGCACA CCCGCGATTA CAAAGGAGCG	480

	GAGGIACOGA AATTATOGAA TGATCTCACC AGAGAGATOG OOCTCATGAA CTTAAAAAAC	540
5	TACACTAGCA COGOCTATGA CTCCTTTGGA CATATTATOG CTGGATATGC TGCTGOCTAC	6 00
	TATGOCTACC TITIGGTCCCA GGTTTTTGCT GCAGATATGT ACGACACAAA GTTCAAGCCC	660
10	AACCCATTCA ATGCTACGGT GGGTGTGGAA TACAGGGACA CTATTTTAGC TACCGGTGGA	720
	CTT	723
15	(2) INFORMATION FOR SEQ ID NO:840:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 692 base pairs	
20	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1531UP	
30	(A) CAUSTALIST PARTITION	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:840:	
35	CATCCAATCC TECACCOCC TTAAACTECT CCTCAATECA COCCACCOCC CACTGCACTA	60
	TOOCACOGAA ATCGCACTCT GGAGGAGGCG CGTGGTTGGG AACTGGATCG TCCACCTCGC	120
40	GCAGAAAGOC CGTTTGGAAG GCGCAGOCGA GGACCGGAAT GAGCATTAAT AAAGAGCTAA	180
	CGIGCATGCT GIGAACAGIT TCACTITATG CGTTGCATTC CTCCCCCCCT GAACACGAAA	240
45	ACACOGCOCA CATOCOCTAT ATATACCCUT COTGTCTACT ATTGTGCGCT GCCCGCTCTC	300
50	ATGTCAGTTT TTACTTTTTG ACGCCGGGAA CGCGACATCT GCCACAACGC ACCAACGCC	360
50	AGTGACCAGC TCTATGCCGC TTGCTCTGCC AATAACCAGC CCCCTACTAG CCGAGCATTT	420
55	TOCCTTAGTC CACCAGATAT TOCATTGTTA TOGTTGCTCG CCAGCCTCGG CCTGGCACAT	480

	AAAGATOOGA AGCTOCTIGTIG CAAAACCTIGCA CAGOOGOGOCT TOGAGAATAC TOOOGCAGOGA	540
5	CCCCCCCCC CATTAGICCT TOGCAGTTTT TTGCTTTGTC CCGCGATAAT GTATCTAAAT	600
	ACAGAATATC GATTACOCCG AATAGOCAAG TTTTGTCGTC TGACATGCCG AGTGTCAGTT	660
10	CATGATTACA TAATGTGTCG TGCCATATCT GI	692
	(2) INFORMATION FOR SEQ ID NO:841:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAG1532RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:841:	
35	GATCTICTICA AAGACTAACC ACCATCAACC CTGCCGTATA GCCAGCGAAA TATGCATATG	60
33	ANGICITICI COGIOGOCIG TITCANTGAC TICAGIGATA TOCCATOCOC AGITTUTATG	120
40	TCAAACTTGC GCCACTGCAG ATAATCAAAT ATCTCCTGCT GCAACACTGC CTGGTAGTTT	180
	TTGTCACGGA GAGGTCGCGG GTCGCGGGTTA CTCTGCAGGG CACGGTAAGC TGACGGACCC	240
4 5	CCCCCGGGAA CAATCGAAGG CCCCTGCGAA GATCGCAGAC TCCGCCGGAG AGACTTTCGC	300
	ACCICCOCCA CAGGICITGA AAGAGACCIC COCCCUITCC GIGCCAGACT CITGITTATC	360
50	ATGICOGIAA GAGCAGCGIT CGICCCAGGI ACGCCCTICT TGITICGIGIT TCCACCAATT	420
	GATOGAATTT GAGACGIGAA CCTCTGCGGA TICAAGCTAT TGAGCACACC ATTGGCACCA	480
5 5	CTTCACCCCC TTCCCTCTCC CATCCCTAAT CCTCCTATCC TACGCCCCC TAATAAGTTA	540

	The second relocated Algerrated Cigana Algerrated	600
5	TCACCOCATO GAAATCATOS AGTACCAATA ACCACGIGAC CATTATTCAC GIGATGAATT	660
	TOCCOCTOCC TOTTOCCGAC TCTTACTCCA OCTTAACCAT GACTAGATOG OCATACCTCA	720
10	GA.	722
	(2) INFORMATION FOR SEQ ID NO:842:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 619 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) Original Source:	
	(A) ORGANISM: PAG1532UP	
	, , , , , , , , , , , , , , , , , , ,	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842:	
35	GATCATCTGA ACOCTCATCA ACAGTTCOCG GAACATOGTG TOCACGACTA TOCACTOCTG	60
•		
	GATGTCCTTC TCCCCCAAGT ACCCCCGGTC CCCAGCAACA ATGTTGACCA CCTTACCAAC	120
	CACCETORCE ACACCECCEA ACAACCETOG ACCEGTOCACA COCTOCACCA TCTCCCTCAC	180
40	The state of the s	100
	GCCAAGCACC CACACAAACG GCCCGCGCTG CGCCTCCAACC TCCAGTGGGA TGCCGCGGGG	240
		240
	GTACATTTOC GOGGGAGAGG GAGCAAAGAG CAGGTOCACA COGGGCTCTT CCAGCAAGGC	300
45		
	SCCATCOSCT SCCAACGTOC TOSSATACOG GTCAAGATCT TOGTTCGGCG CAAACTGCGA	360
50	AGGGITTIACG AAGACTGAGA CAACAGTAAA GIOGITTITOC GOGCACGATC TOCGCACGAG	420
	CGTCATGTGT CCCTCATGTA GOCAGCCCAT CGTTGGCACA AACCCAATCG TCTGTGTCTT	480
55	GCAATCTACC GTCTGCTTGC GCCATTGCGA GACTTCCTGG ACCTTATTGA GCACGTGCAT	540

	CARRETAIC GUITICATES TICARCUITE AASITISTER GISTOCATET CARACATTAA	600
5	GGAAGCITGC GCACACIAT	619
	(2) INFORMATION FOR SEQ ID NO:843:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 564 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genanic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1533RP	
	(II) CARRELLA PROIDURE	
25		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:843:	
30	GATCACGAAC TOCATCATTA CAAAGTOCAT COCCTOGATA CGAAAACAAA ATGCACAGCC	60
	GCTACCCACC TTCCCAAAACC TCGAGAAGAT CAACCAGCCG CCAAAGAACG CTGACCATGC	120
35	GIGGGAGIAC ATAAAATCGT GAATTATTGG GGITGTATGT ACTATATACT ATCGCTCTGC	180
	OGCOCAATGA TOGITACOCC TCTTOCACTG GCATTCTGGG TGACGAGGTT GTCTCCGTAC	240
40	ACCTCTACTA TTTCCAGGIT GGGCGCACAT TCGCTGATAT GGGCGAGCAA TTTGTCGTCA	300
	ACGCAGCGGA CGAACCCTAC ATTCAGTTGC TGCAAGTTTG GACAGGACAT TAGCTGGAAC	360
45	CCASCIGCCG TCASGITCCT GGCTGAGTTC AAGITTAGCT CTTTGAGGAA TTTGGAACAT	420
	GGATTCAACC ATATCTCCGC AATTGATGCA TCATCCAGCT GATGGCAGGG CCTCAAGTTG	480
50	AGGTAGTGAA GTOOGGGAAG CTOGACOGAA GAGAAAAATG TAATGAATOC ATOOGACGTA	540
	ACCTOGROCA ATTCCTCTAG GGAT	564
5 5	(2) INFORMATION FOR SEO ID NO:844:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIH: 720 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
_	(A) ORGANISM: PAG1533UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:844:	
	CATCOGGAGA CAGACGIGIA TOTGAGITOT ACCOCTOGGC GOTGAAACGC ACGTOGTTAG	60
25	COCACATOCT GIGIOCTICC ACCOCCCAG ACCAACCAAG TATTOCTATA TICGIGAAAA	120
	CTGCGGTAAT AACCATGTAG AAGATTCCGC GCCCGAATAC CCGTTTTACC CCAATATGTC	180
30	CGICATGICA GCTATTOGAT CGAAGAGITT TIAATGACGI AICCCCTATC ATAAAGCGGI	240
	OCTOGATTAT TOGAGCATOC ATCTOGTTICA OCTOGGGCGT OCCAAATATA TOGTOCAACA	300
35	AGAAACTATC GTACCAACCC CGTCTGTTCT GACCTGTGTC CTCTTAATCG GCATGACTAA	360
	TATGGGGTAT CCTTAAAAACC TITAAGATGT TACCTCCGGT CTCCAGGGGG GFTGTCTAGT	420
40	TTACAAGAGT AAATACCACC TTGCCCCTGG GAGGGFTCTT ACTTTACAGT AGGAAAGAAT	480
	CGATACCACT GGIGGGGGA TITGGIATAT TITGAAAGAT GGATGGAATG GAGGGCTCCT	540
45	TATTGACAGC AAAGCCACTC CGACAGAATA CCCACACCTT GGATTTGGAA GCTGCGGATC	600
	GACAGAACAT GGTTACGTAA TCGAATTGTC CTGTCGGGCC GCCCTTCCGG TTAATCAAGA	660
50	AGAACAACCG CGGGGCACGC AGGGAACTAT TGAATTCAGT GCTGCCAAGC CTAATTTATG	720
EC	(2) INFORMATION FOR SEQ ID NO:845:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIH: 727 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1534RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:845:	
20	GATCCACATT OGAATATOOG TATOOGACTT GATGGTTGAA COCTTOOCTT CAACCACTGC	60
25	AACATTOOCA AACCOTTICA AGTOCTOCAT GATTTTCTCC TICTOCATOG CAGTCAAGAT	120
	GIGGCCGAAT CGITTTTCGT TGTATAGGCC TIGCTCATCC TGTGCTTCAT CCTCATCAGA	180
30	COCTAATOGA ACGICTOGCA CAATCICGAC OCCATCOCAG GATOCCATAC TCAAGGIATT	240
	GAGCATGITC AAGOCATGIT COUTIGCTAC TITAAACOCT GCATCAACIT CCTCCTCGIT	300
35	TTTCCATAGG CCAGGGACAT CGTTTTGATC GTAACGAAAC TTACTTTCAA AGCGTTCTCT	360
	CAGIATAGAA ACCACATTGT CTTCCTTCAA ATACTGGIGG ATAATATCAT ACAGAATAGT	420
40	CCATGCATTT GACCGGATCT TCAGGTATAA AGCATAATTG TCCTCCTCGA TGAGGTCGAG	480
	CTOGAAGICG TAAGCOGTAC TITICATCOCT GACATCCCCT AAATIGGGTA GTITATACTT	540
45	TAGAACTGAA COGCOGAAAA CATCATCAAA GIGGICCATA ACAAGTTGCC AGACGITATC	600
	CIGIOCATOS CACACTAAGI OCACAATATO GICTOTAGIA TGIGICAATT OGIACTITIT	660
50	CGCCCTCAAT ATAATACCTT TCATCTCCTT ACCACGCTCT CTTTCCCCTA GTTCACTATC	720
	TTCTCCA	727
	(2) INFORMATION FOR SEQ ID NO:846:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 682 base pairs	
5	(B) TYPE: nucleic acid	
J	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1534UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:846:	
20	CATCAGOGIC CACTICATCA TOGICICICI OGTOCOCCCC TGTCGTAGGC GGGGGACGCT	60
	GCTGCTGTCC TTTGTGCGGC CCGCGGGGGGC GGCGATCAAA GAIGGGGGAC CACGGTGGCC	120
25	GCCGGGGGGG CTCCAACACA CACGGGGACA GCAGGGGGG CGTGCCGGGC AATGCAGCCC	180
	GCACAGCTAT CCTCCCCCCT CGTACCCGTG GCTGCCTTCG GCCGGATTGC GCTCGTCAGC	240
30	GETCACETGA COCCAGATAT GITGCAAACC AAGCCATCGA TOGGCATAGG AACGCATTAC	300
	CAGCOGATTIC GAAAACCCTC ACAACCCCCC ATCTGCTGGT ACCACCACCG CAAGTCGCTG	360
35	SCACTOSTIC CACASTOSTA ASSICTICOST TCAAAATTAC TCTGCCASGG COGCTCTCAA	420
	AACCTOTCAA GTOCAGACGC ACTGACAGTC CGTCAAGATG CGACATTACA ATGCTCTGGA	480
40	ASCICIOCAS TAGGITICTOS COOCCGIGCT ASACAGICAS GOCCAGOCTI CATOSACAAA	540
	CACCCCAAG GATGTCCCAA TTCGTTCCCA CAGTCCACTC TAGCGTCCGCA CGGGAAAAAC	600
45	ASCOCTACTO TOCGTTGACT GOOGCGAGAC TOCTAGCOGG CTGCCGTGGCC TCAATCAGGA	660
	CACACCAAGG TGATCATGAT AC	682
50	(2) INFORMATION FOR SEQ ID NO:847:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 663 base pairs	

	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOCY: linear	
5		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1535RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:847:	
	GATCTTOCTG CTATCCAGAA ATGOGAAGTT CTTAGACAAC GGGGAATTAA GCCCCTTTTC	60
20	CAATATITIG ACCGICGITT CATACCTCCG AACACCCACC ACAACCCCCC CCACTACTCT	120
	CUSTICATET TOOCICATEA AASSIGICIC TATCAAATCT ASCICCATCA TOSCAGASTA	180
25	GITATTATCT TTCTTCCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGGA TTACAGTAAA	240
	ATAATUGTIAG AACCOCCGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCGTA	300
30	CAACATOGIG COCCCCIOCT TCTCTATCAC AACATGCAAC TGCGAAAGTC TGTTCACGGG	360
	GCACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
35	CCGCGCGAGC TCAGTCTCAA GCTCGTCGAT CCGTCGCAGC AGCTCCACAT TCGGCGTCGA	480
	GCTGAACAGC TCCCGTGAGT TCACGTCGTG CGTAAACTCA GACAGGTACA CACACTCGGG	540
40	CACCCCTTC CCAATACATG TAGAGCACTT CGGCCGCGCC TTGTTGCACT TGACGCGCCG	600
	CTTGCGGCAG AACACGCACG ACTTGCTGAC CTTGCGCCTG GTTTTCACAA TCTTGCCATC	660
45	ASS	663
	(2) INFORMATION FOR SEQ ID NO:848:	
50	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 649 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

1105

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1535UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:848:	
15	GATCOCOGAC GTGGACCACT GOCCOGAGAT GCGCGCGGCC ATCCTGGTGG TTTCTGCGGA	60
	CCCCAAGGAC ACGCCATGGA CGAGCGGTAT GCAGCAGACG GTGCACAGGT CGGACCTCTT	120
20	CAAGGAGCGC GTCCCCGACGG TGGTGCCGGG GCGGTACGGA GAGATGCCGG CGCCCATCCGG	180
	COCCOCCAC TICCCCACCI TICCCCCCCCI CACCATOCAC CACTOCAACT CCTTICACCC	240
25	CACCIGCCIG GACICATITC COCCGAICIT CTACATGAAC GACACITCOC OCCGGATTGT	300
20	CAASCIGIGI CATCIGATCA ACGAGTICTA CAAGGAGACC ATGGTGGGGT ACACGITIGA	360
30	COCCOCTCCC AACCCCCTCCCCTCTTATTACTT COCCCCACAAC CAACCCCCCC TCTCCCCCCTT	420
35	CCICICIOCC GICTITOCCG CCAACGACGC CTGGCAGACC ACGTTCTGGA CGCAGCAGCG	480
	COCCACCITIC GCCCCCCACT TCGACGAGTG CGTGCGCCCC AAGCTTGCCAA CGCACTGCAC	540
40	GACCAGTTGC ACAGAGGAGT TGCCCGCCTC ATCTTCACGA AGGTCGGGCC AGGGCCCAAG	600
	ACACTAAATC CTCGCTCATC GACCCGAGAC GGGCCTTGCC CCGCCTCAC	649
45	(2) INFORMATION FOR SEQ ID NO:849:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	()	

	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1536RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:849:	
10	GATCATTIGT CCTTGCAGCA CAAACATOCA CAGCTGTCGC ATTIGCAGTT GCAATCCGGA	60
	OCASCASCIC CITOSCASCA TITOCAAACG CCASSCICTIC CCACCICTIT COCATGITCT	120
15	TOTESACATIT TIGHTIGHTO TAAAHOGIGA THITESAGIOG AUGGITOOGA GACOGOOGGA	180
	OCTGACTATA GOODGCACCA AGACCCTTTA TATATTITICG CAACCAGATA CATTAATIGCG	240
20	ACCICARARC ACTATCARAR ATRACCIATRA GOCICATTIT TRITICICACO CATCOCACAT	300
0.5	GCTGTAATCG GATTATTCTA ACTAAGCTAG TATTATGTCG GTATCCTTTT ATTAATTACA	360
25	ATCACIOCTE AGITOGOGIA TOGIOCAACT OCACACOCAG CTCATCAGIG GITTOGITCC	420
30	COCOCAGATO ACOTOCCTOC GACATOSOGA CTTCATOCAC TOSOGOCCAG CTACGTOGIA	480
	TATGACATTA TOOCCGAGAG GITAAGGCGT GAGACTCCAA CTAAATTCAG GCATCTCTTG	540
35	GOCTICTOCCC GCGCAGGTTC GAATCCTGCT GATGTCGTTA TTTTTTTGCTT GCGCGGCCTA	600
	COOGGOOGIG TATTICCTIG TICCTATTIA CATAAACCAG ATACTAAACT ATCCGTAGAA	660
40	CICOCOGIAC TICCOGIAGI ACTACOCTET CCCGAAACCG CCCAGGOCGG TGAGCAC	717
	(2) INFORMATION FOR SEQ ID NO:850:	
45	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 710 base pairs	
	(B) TYPE: rucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1536UP

(xi) SEQUENCE DESCRIPTION: SEO ID NO	5·850·	ID I	SEO	DESCRIPTION:	SEQUENCE	(xi)
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5	GATCADCIUG GIACTOCAGA AACAAGOCTA CIGIOCCTIG CCTIGACGAA GITACOCGAA	60
	ATCCAAAGCA GCAGCAACAA GCAACATAGC AAGACCGCTA AATACATTCT CAAGTCATTG	120
10	GAATAAGCTC TAAAACTACC GATACGTATA TTTACTGCGT TAACGTTTAT ATACATATAT	180
	CTACOCCIOC GIATOGGIGI IGIACGIGIA CATCIAACCA AATAACICCA CIATACCIGI	240
15	AGTACATOGC ATTCCCTTGT AAGCAACTTC AGGTTCTGGA CTACCCAATT GCTGTCCCGC	300
	ATCCCAGCCT TGGGGTCGTG GCCCTGTGTT GACCTCAATT TAGCGAAGAC GGACTTGTAG	360
20	TOSCICICAT ACTOCITICAA TTOSCICAATG ACGOGGITAG AGTOGAACTIC AACATACACG	420
	COCCIATOCA CIATOCTICAA GAGGACATOG TOCACACGCA GGAAGAAACG ACTCAAAATC	480
25	AGCATACACT COTTCATCAC TCTCACCTTA ACATTCAGAA TGCTAATGCC ATTGTCCGCT	540
	ASTROGRACI CAAATAAAAT CATGROGROG TAGAAAAGAA TOOGGROCOG GCTCGAAAAG	600
30	CITOGOCAÇA GOCAGOTOCA COCTIGOGIC TOTGACCATO GOCOTIGOCAT CTATOGIGOC	660
	CTOCTAGAGC GICGTGTACG TCCAGTCGTA CTGGTGGGAT ATGTTTAGGG	710
35	(2) INFORMATION FOR SEQ ID NO:851:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 737 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	

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- (ii) MOLECULE TYPE: INA (genomic)
- (vi) ORIGINAL SOURCE:
- 50 (A) ORGANISM: PAG1537RP

(xa) SEQUENCE DESCRIPTION: SEO ID NO:89	(ici)	SPOUFNCE	DESCRIPTION:	SEO	TD NO: 851
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GATCTCCGTA	CTTTAGGATG	GCTTTATAGA	GGGCACGAAT	TICCCITICG	CCTATAGAGT	60
TCAGGITGTT	GGATTTCGCA	CGTTTTTTCG	AGCGTGAATC	CICITICICG	CITAAGCICT	120
GAGCTCCATC	TCCATTGACG	CTATITITA	TCTTATTCAG	AGCAACATTC	CTACGATTCA	180
TCATTTGCAG	TIGITCCIGG	ACATACICTT	CATCCTTCCG	CITCIGITCI	TCGTCTTTCA	240
GITIGCGIAG	CICGICITCC	OGAATGATAT	CATCCCATTC	CACGICAGCT	TTATAATOOG	300
TGACTTCAAA	CTGTTTTAGG	AATTOCTCAC	CTCCCAGATG	AGACTOTOCO	AAATCTOGTG	360
TGGTGACGTG	ATCTTCCGCA	TGATTCAAGA	CATCATCCAA	GTTCAAATCT	TCAAGCTTCT	420
TTTGATTATC	ATGCCCTTTG	AACATATTGC	CTGCACCAAA	CITGAGAATC	TCAGACAGCT	480
CTCCTGCACT	AGGITCOGCT	TTGCTCTTGC	TOSTATATIT	ATTCCCATCT	GTAACACCTA	540
ACCACATCAT	AGCATACTCC	AAGATCATCT	TITTOCGIGC	TCITTCIAAG	ACFICTICIT	600
CAACGGIAIT	CTTAGACACA	AAACGGTAAA	CCATAACATG	ATTCTTTTGA	CCAATTCTAT	660
GCCCCCCACC	CATTGCTTGG	AGATOGGCCT	GTGGATTCCA	GTOGGAATCA	AATATGATCA	720
CAGIGICIGO	CGTCATC					737

(2) INFORMATION FOR SEQ ID NO:852:

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35

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15

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genamic)

50

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1537UP

	SEQUENCE DESCRIPTION: S	1D 10.65	2:		
5 GATCTAGAC	C ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	A TACGAAGTAA	AAGCAGTCGG	CACCGICIT	60
CTGGCAACG	A CONTINUITO TACACACCIN	CTOOCACAGG	ATCCAGCATC	CTGCCGCATA	120
O ACGTCAACO	C COOCCEPTOR ATGGFTCCC	A GGTGCCACTG	GCGCCAACCG	CTGCGTGAGA	180
AACAGCAGC	G CTOCACTICG CTOCTICCO	GAGGCICCIG	GAGTGGTCC	CCCCTTTTG	240
5 CCACCGCTC	A ACCTAGOGGG GCGTCGCTG	r eccesserici	CCATGCAACT	G3GGGGGTTCC	300
CATGATOGO	G GOGOCCTTAC CAGOGTOGTO	TTTGGGCTGC	crescrerec	CTCCCACAC	360
CATOSCCTO	C TOGAGGAGCT GAACCTGCT	r costostoca	AACCIGICIC	CCACACCCCA	420
ccroccroc	A ASCTIGIOCCT GCGGGGGGCG	r grogartoct	CCCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	GIOCAACTGT	480
es Cottgacaco	G CTTTGCAGGC ACGTGATGG	г тостосског	CCCACACCIG	CICGGIGIGI	540
	C TITICCOCOG GCTGCGGCC	COCCETTOCC	OCCATATCAT	TGATTCCGTC	600
00 TOGATTAGIN	G CATOGTOGTC ACCTTOCAG	A TOSCCAGOCT	GIACTIGIGC	TTGCCCCGGG	660
	T CITIGOCIGI GCCGGIGGG	r criccitgic	GEOCTIOCO	CGITCT	716
es (2) INFORI	MATION FOR SEQ 1D NO:8	53:			
(i) :	SEQUENCE CHARACTERISTIC	CS:			
10	(A) LENGTH: 733 base p	pairs			
	(B) TYPE: nucleic acid	£			
	(C) STRANDEDNESS: sing	gle			
	(D) TOPOLOGY: linear				
(ii)	MOLECULE TYPE: INA (gen	nomic)			
(vi)	ORIGINAL SOURCE:				
50	(A) ORGANISM: PAG1538	R.P			

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:853:

	GATCCCICIG CTACAAACAC ATACCTAGAT TTCTCATATT TTATACTGAA TACATATAAT	60
5	ATATCATTTA ACTOTOTICA TICATGAGAC GIOGICIAAG TICTGIOCIG CICAACTTGI	120
	TITTICCACTT GTCAGCCTCT TCGCCCCCCCA GTACGTTCAC CACATGCACG GCTAGCTTCC	180
10	TCATTCCTTT CCTCTCACCC GTATCGTTGA TTGTCTCCCC ACCCCCCACA GTTTCCTCAC	240
	TCACTACCAG GOCTTOGATA CCAGGITTOGC TACCOGTGGG CCCGCACACG TCATGTAACG	300
15	CAAATATTIT GATTIOCAGO COOGGITTCA GOOTGIGAAG GAAGOTGCAC ACGITATOGO	360
	ATCCTTCCTC GAACGACTGA ACCTCCTCCC TGTATTTCTT GTTCCCCAGC AGTTCTTCAT	420
20	CTGTAATCCC CACGATCAGC COOGACOCAG TCACGAGCOC GOCAACACTG AGCAATATTT	480
	TATUTOGIC GIGHAGIGG TOGANAGIOC CICCCAGOOC GCTAACAGOG TACTIGICIC	540
25	TACCOCCACT CTCGACCOCC CCCCCAGCCG CCATCGCCGG ACTATCAAAC AGCTCTATCT	600
	OCCUCATORS CARCOCATOR TOCASCAGOS CATOSCICAS CARTACAROS TOCCACITOR	660
30	TICOSCIGIA COCTICCATA CIGACGITGA ACAAAACATT TATCGGGGIC GIGIACAGCT	720
	TCTGCTTCAG AAG	733
35	(2) INFORMATION FOR SEQ ID NO:854:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 725 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1538UP	
50	(c) Unimitation Emiliations	

(xd) SEQUENCE DESCRIPTION: SEQ ID NO:854:

	CATCCTTGGG ACCACATCGA CACCATTTCT ATCGGTAACG AACTTGTGAA CAACGGCCAG	60
5	GCCACCGTGG ACCAGATGGC TGGTTACATG AAAACTGGCC GCAAGTGCCT CGCTGAGGCC	120
	GOUTACAAGG GOOCAGITGT TTOOGTGGAC ACTITICATOG CTGTAATCAA CAACOCTGGT	180
10	CTATGTGACC TATCAGACTA CATGGCTGTC AACGCCCACC CATACTTCGA CTTCCACACT	240
	TCTCCTCCTA TGCCCCCCC TTGCGTTTTG CACCACATCC ACACACTCTG CACCCCCTGC	300
15	AACGGTAACA AGAAAGITGT CATCACCGAG ACCGGCTGGC CTACTCAGGG TCAGACTTAC	360
	GOCAAGGCCA TICCATCCAA AGCCAACCAG AAGATGGCCT TGGAATCTAT CAAGGCCACT	420
20	TGTGGTGATA GCGCTATCCT ATTTACTGCT TTGGACGACT ACTGGAAGCC AGATGGGCCT	480
	TACOGIGICC ACAAGITCIG GOGIAICCIA TAAGITCCCG TGICCTICTT TATCACCIGI	540
25	CICITIATIT TOCTOGGAAC OCTTACATOC AGATOSOGGG TGGCGGIGCA TGGCCCTGCA	600
	GOCTICCOCOC CTGCAAGTTT CTACATCOCC CTACTTTACC TGCCACGOCA CTTTTGAATT	660
30	TCTTTGGCAC GTGGTACTGC TGGCATCCTT CTCATAGAGC ACAGTGTGCC ACAGGGTATC	720
	ACTOG	725
35	(2) INFORMATION FOR SEQ ID NO:855:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1539RP	
50		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:855:

	CATCACACAT GETERTITIC COCCETCOCT COTTETOCCT COCCECACCE CACTICACTE	60
5	GOCCAGCATC AGTITITIGGIG GCAGCAGAAA CCCITAGGAA TGTGACTITIC TCTTCGGAGG	120
	AAGTGITTATA GCCTAAGGIT ATACTGCCAA CCGGGACTGA GGACTGCGGC TTCGGCCAAG	180
10	GATOCTOGCA TAATOGITAA ATOCOGCOCG TCTTGAAACA COGACCAAGG AGTCTAACGT	240
	CTATGCGAGT GITTGCGTGT AAAACCCGTA CCCGTAATGA AAGTGAACGT ACGTGAGCCC	300
15	CICITIAGAG GIOCATCATC GACCGATCCT GATGICITCG GATGGATTIG AGITAAGAGCA	360
	TAGCTOTTOG GACCCGAAAG ATOGTGAACT ATOCCTGAAT AGGGTGAAGC CAGAGGAAAC	420
20	TCTGGTGCAG GCTCGTAGCG GTTCTGACGT GCAAATOGAT CGTCGAATTT GCGTATAGCG	480
	GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTTCCTGCC GAAGTTTCCC TCAGGATAGC	540
25	AGAAGCTOGT ATCAGTTTTA TGAAGTAAAG CGAATGATTA GAGGTACOGG GGFTGAAATG	600
	ACCTIGACCT ATTCTCAAAC TITAAATAIG TAAGAAGICC TIGITGCITA ATTGAACGIG	660
30	GACATATGAA TGAAGAGCTT TAGTGGGCCA TTTTTGGTAA GCAGAA	706
	(2) INFORMATION FOR SEQ ID NO:856:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 743 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1539UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:856:	
55	GATCACTACG TGACATTCGG TACGGAATGG CACTCCAATG CCGACAAACC TCTTCCTACC	61

	CONTRACTOR CONFINED CAMPACTURE CONTRACTOR ACCURATIONS	120
5	CACCAAATGT ACTOGATATC GTTATTACAT GTCTACGCCC TCACGTGCAT CCACCATCTG	180
	ATATCATGIC TOCTCTAGGC TATATATTIC GGTTGCGGCC ATATCTACCA GAAAGCACCG	240
10	TITOCCOGROC GATCAACTOT AGITAAGCIG GIAAGAGCCT GACCGAGIAG TGTAGTGGGT	300
	GACCATACGC GAAACTCAGG TOCTGCAATC TTTTTTTTTT CCTCCTCCTG CAAGCTGGCC	360
15	GCCAACACAG GTCACCCTAG TATGGCTCAC ATGCAATTCA GATATCTACT TCTGACTGGT	420
	CTOGTOGGCG ATCGCCATCA TTGCAAACAG TGTGCTCGCA TGGGACTTTA ACGACCTCGC	480
20	GATAATAATC AGAGATCGTC TACTTATAAA ACATCAGGCA CAAAAAAGAAA GGTGCAGCGA	540
	AATOGTATAT ATAGGTOCTC CAGATCCACC ACCGGTACCT CCTACTTGGC CGTATCTGCG	600
25	TOTOCGTOGC GCTTGCCGCT GAGATGCTGT GGGCCCGAAA TGTACTCTCA AATGGGCTTG	660
	TTCAGTGCCC CATACAGCTC ATAAGCTCAG TGCCCCCGAT GCTTAGTAGT ACCTGCCCCG	720
30	CICITCATAC TOCTGTCTGT ATA	743
	(2) INFORMATION FOR SEQ ID NO: 857:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(Vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1540RP	
50		
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:857;	
F.F.	GATCITITCT TIGICAAAGI TCAACACCIG TAAGCCGCCT CTAGATACCG CTCTAGAAAG	60
5 <i>5</i>		

	GOCCACATAC OCTIGOCCCT TITCAAAAAC ACGICIGAGA TCCACTITICA CTITIGITIAG	120
5	TGTTTGGCCT TGAGATTTAT GAATGGACAA GGCCCATGCA AGCATGAGTG GCAATTGAAC	180
	TOTOGITACT AGAGOCITOT CATTITOGIC CITOGATAGOC CATGOCICIT CITOGAACTAA	240
0	AACTOTTCTG GTGGTATTGT CGGGCTGGAA GAATTGCACT AATGGCAACT TCTTACCCTT	300
	TGAGCTCATC TGAACTFCCT GTAAGAGCTG CTTCTTCCGT TCTAGATTGG CCTTCACTTC	360
5	AGGATCTGTG ACTTCTCGAT CATCCTTTAA GAAATCGAAT ATCGTGTCCC CCAAGTCGTC	420
	TACAGIGICA TCIGIGICIA TCGICCIAAA CTICTCTCGC AGAGCIITCT TGACCATGCT	480
20	TETECOSSTC TOCTTCTTGG GCTCCTCATC CTCATCAAGC TCGGGGGGGT TCCAGTCGTT	540
	TITOGCTAAT GCATCOCGAT ATTICTCCCA TICTGCAACG TCAACATCAT CATCGCCAAC	600
25	ACTITICATAG AACATAAATG TIGOCTICATC GATGAAGTICA ATGACCTTCC OCAGTGATCC	660
	GITTACCACT CHATCATCCA ACTTCTTAAT CITCATAACC TGTGCGCCCA CITTAA	716
00	(2) INFORMATION FOR SEQ ID NO:858:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGIH: 643 base pairs	
-	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1540UP	
.5		
50	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:858:	
	GATCTOCTOC GCGAAGAGCA CGCCCTGCGC CCATCCGGCA TAGGGGCCCC ACTTTTGTAT	60
55	CAACATTICC COCACAACCT CCACCTCCAT GTTCAGTTTC TTCCCCACAC TCCCCAACCTC	120

	CTTGTATCGC GCTTTCAGCG CAGCGATCTT CGCTGCCGAT GCATTGAACT TGTAGTCTCT	180
5	THE TOCKART CHEFT COACCICIAL ACCORAÇATOS TOCHOCATOT COATOCCCAT	240
	CACOCAGACG CAATICTOCGA COTTOGGACC CACOCOCGGA ACCTOCATAA ACCOCTGACG	300
10	CATCTCCTCC COCCATATCA TGTCIAGCCA OCATTCCAGG TGTTCAGTAT COCTCATGTG	360
	TOCCOGUITA CUTGAATOCA TOCATUCTOC OOCAGOCATG ATATACUTOG COCCATACOC	420
15	AAACCCCAAA TCCCGCAGIG CGTCCTCGCT AGCGCCTTCC ATCAGCTGCT TGCTGGTGGG	480
	CAATCACTAC TATOCACTAC OCTOCACCTO COCCACAGCAAC CTOCCCTACT COCCAACACAC	540
20	TOCATOCCAC ATCTTCGTGA TOCGCCCCAT ATTGTTGTTG CTAGAGCAAA TAAACGAGCA	600
	CASTGICTOC CAGGGTTCCT GTCGCAGIAT TCGCACGCCA CGA	643
25	(2) INFORMATION FOR SEQ ID NO:859:	
	(i) SEQUENCE CHARACTERISTICS:	
3 0	(A) LFNGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) Original Source:	
	(A) ORGANISM: PAG1541RP	
40	(A) Crashvish: PAGIS4IRP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:859:	
	GATOGAACAA CCATACTTIA GOCCCACACG ACCGTTCCCC TOGGGGATAT CCTGCCGCCC	60
5 <i>0</i>	CTCTACAAGA TIGGATTCAA TCATCACCCC ACAAATGGCA TTCTCACCTT TACTCACCTG	120
	CICATAGATA TCITIGGGGGA CITTCOGCTG GITGCGGTAA TCCTTGTTGG AATTTCCATG	180
55	CGAGCAGTCA ATCATAATCC TOOGCTGGAC CCCAGCGCTG TCAACTAGCT TCGCATTGAC	240

	CAAGUCCUGC TUAGCCUGUT GUACACUGGC AGCGUCATAG TUUGUGCCAT CUTUACCACC	300
5	OCGTAGAATG ATGAAGGIGT OCTOGITACC TTCAGTCCCA ACAATCOCAG TCACTCCAGG	360
	CTTOGTAACC GAAAGAAAGT AATGAGAGTG AOCAGCOOCA COCATAGCGT CAATAGCAAC	420
10	CTGTAAGCAG CCATCTGTCC CGTTCTTGAA TCCGATCGGG AACGATAGTC CAGAAGCCAG	480
	CTCACCCTCC ACCTCCCATT CTCTCCTCCC CCCCCAATC CCCCCAACC ACAACCACTC	540
15	OCTTANGANC TOCOGOGATA TOGTIGTCTNG CATTTCGCCC GCANTTGGAN TGTGCTCCAC	600
	CASCISCISTS TACATOTOCO SOCRAGATACS CARTOCOTTIS TITATTTOCA ACGARITATO	660
20	GATGICOGOG TOGITGATGA GCCCCTTCCA CCCCACCGTG GTCCGCGGTT TTCCAGATAC	720
25	(2) INFORMATION FOR SEQ ID NO:860:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 732 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1541UP	
40		
	(-1) CD2 TD 10 CC2	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:860:	
45	GATCAGCTICA TIGAAGATTIGT ACGTICATICAC TIGCTIATTTIAA CACAAACATA ACATAATTICA	60
50	TOCOCCATAG TITAATCCTT AGAATTCCCC CTTGTCCCCC GCCGGATCCG GGTTCAATTC	120
30	CCCGTCCCCG ACCTITITGT CACATTIATT CAAACCCTTG TCGTTATAAC CGTTCCCATG	180
55	GAATGTGGCA GCACCCTGTA ACGGCGACGT ATCCTGCAAC TTGGACGTGT TGTGGGGTCT	240

	ACCICACICE TICCOCCTICC ACAAATICCC TITCCCCCAC CCCCACITIT TGTCACCCAA	300
5	TATTIGAGCI CCIGATCATC AAGCICTAGI COCACACAGG COCCCCAGI ATCCATTGAC	360
	AAAGGTCGGC GCAACATCCG ATCGCCGGGT CCCTTTATAT ATAAATATAC ACTAATCACA	420
10	CATOCGAATA CCCGACTOCC GTOGATAGGG GACGTTTGAG GCCTCATACC CCTCAATACA	480
	CATAACAAAA TIGGAATATA GGAGAAGAAA TGITGGAGAG GCTAAAACIT AGGITGCGGC	540
15	CATOCAGAG ACTCAGAGCC AACCGITTIAG CAGACGITTCC ATACCCGAAT CCCACGITIGA	600
	ATTOCOCAAT CATTTOCAGA ATOGACACAA TOAOGGTGTC AATOTOGGG OGCTATOGTC	660
20	CTTGAGAAGT GGATATCGAG TCGATGTTCC AATGTGGGGG CGAGACCGAG CATGCGGGGA	720
	TCAGGAAGAT GA	732
25	(2) INFORMATION FOR SEQ ID NO:861:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 614 base pairs	
3 0	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1542RP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:861:	
	GATCATGIGG AGGAACTOGG GCAGCGTCTC GCAGCCGGGG TAGTGGGGCTA CTGTGGCGGC	60
5 0	GCGGGGCAGCC GACTGCTCGG GGTATTCGGG GGCCGGCGCA GCGGGCGTGTG AGCCGATGCT	120
	CCCTCCCCCC TECCCCCCCC CCAACCCCTC TOCCCCCCCCC CCACCCCCCC ACCCCCACCC	180
55	CCCCTCCCAC AGCCCCACCA CAACCCACTC CACCCCCACG AGCATCACCC TGCTCCCCAT	240

	CONCERNO TICARROCCI CONCERNO GOOTICOCO ARRIGERRO CONCERNARAC	300
5	GCTGATCACG TGATGCGCCCC GGCGGGCCAG CGTCCAGGCG GGATGGCCGG TGACGGCCAT	360
	CACCOCCTG CCCCCGICCCA ACCCCCCCCT CCCCACGTAG CCCCAAGT CCAACACCTC	420
10	GICAGICTOG COGGAGIOGG AGCAGAGCAG CAGGGGGTOG COGTOGGCGA CGATGCOGAT	480
	CTCCCCCTCC ATCCCCTCCC TCCCCTCCAA GACCCCCCC CCCATCCCCA ACCACTCCCA	540
15	GCTCCCCACA CTCTTCCCCCA TCATCCCCCAA CCACTTCCCC CAGCCCACCA ACACCACCTT	600
	GOOGCOOTIOC GOOGA	614
20	(2) INFORMATION FOR SEQ ID NO:862:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 654 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1542UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:862:	
	GATCATTTAC CTACOCATOG GOCTGCCGCG CATTGCCGCA GACGCATCGC TGCGAGACGG	60
45	CTACCTOGAA CACTACTACG AGAACGCGTA CGCCGCCGCC CTTCTGGACG GCTGCCGTGT	120
	SCARCOCCIG ATTAGGACTICC ACSOSCISCIC SCIGITAGOGA GICATIOCCIC TIGITOCCIGGAC	180
50	CCCACCOCTT TOCCOTCTCC CCACCCTCCC CCTTCCCACAAAAA CCACCCCCAC	240
	OCTOGTATAT AAACOOCACA CGAGCCATCC GGCGTCAGGA ATAGCGTGAG TCGACAAGAT	300
55	GOGTGCGGAA CACGGTCCTA AGGACCTTCA GAAGAAGCCT GTGAGCTTTT CCAACATTGC	360

	CCIGGLAGUE GCGIIGAANA IGIGCCASCT CASCACCCCTT GCCCAACCCC TIGAGCICAC	420
5	CAAAACGACC ATGGCCGCAA ACGGGCAGTT CGGCTTTTCG CAAGCGGTGC GGCACGTGTG	480
	GICCCGIGGG GOOGIGTICG GCTTTIACCA GOOGCTGATT COGTGOOCTT GGATTCAGOC	540
10	GTCCACCAAG GGCGCGGTGC TGCTGTTTGT TTCTGCCGAA GCCGAGTACC AGTTTCGGCG	600
	CCTTOGICTC ASCAACTICG GTGCACOCAT CCTGGGGGGG TGTCTGGGGG CGTA	654
15	(2) INFORMATION FOR SEQ ID NO:863:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 714 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1543RP	
30	(1) Committee Examples	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:863:	
	GATICCCTTIAG OGACTICTICIC CACCOCTICGA OGAGGCCATT GAGCTICTTIAC GAACTICCACA	60
40	AACCTACTCG AACTCTGTTT CCAGACTTCT TICTGTTTGT CTTCAACTGC TTTCGCATCA	120
	AGIACCCCC AGGCTATTIT TCTTACCCCC CIGGIGITIG TCTATATACC CGGTTGTATT	180
45	TITIGATAAAA AACTCAGCIC TICCICIACG GCAGAAATAT ATATCCAGTC CTTAGCCCCA	240
	TOCCAAAATC TOCCTTTTTA COOCTGTTTC TCCCAGTCTT AGCACTGGCA GAAAAAAAGAT	300
50	CTATCOCCTA TACOCCCTCC CCCCCCCCAA AAAAAAAAAA	360
	AAAAGACGTG GOCCOCCCG CGGGCAGACG AAGAAAAAAAT AGGCGCCCAC CCCTCCAAGC	420
55	AGACGACAGG CGAGACATAA TAAAATOOCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC	480

	CCGGCCTCAT ACGCTGCCAT TCTGTTCCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA	540
5	AAGCATTIGCT COGACGCTOC GCTGCCTTGC AGTICGACATC CTCTTCCTAA CCCCAGCCAG	600
	ACTICCCATA CITTOCACIT CACATAGCAT ATCACTITIC AGATCACTAC GIGACATTOG	660
10	GIACOGAATG GCACTCCAAT GCCGACAAAC CTCTTCCTAC CCCGTGACTT ACCC	714
	(2) INFORMATION FOR SEQ ID NO:864:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 680 base pairs	
	(B) TYPE; nucleic acid	
	(C) STRANDELNESS: single	
20	(D) TOPOLOGY: linear	
	(5) 10203001. 223000	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	Lil Objects	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1543UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:864:	
35	GATCCGTAAC TICGGGATAA GGATTGGCTC TAAGGATCGG GTAGTGAGGG CCTTGGTCAG	60
,,,		
	ACCOURGEAGE TETECTTETIC STETISTECTIC GOOGGETTEE TOUTGOOGAE GEACTICETTS	120
	CONCOUNTS CONCACCOC CONCOUNTABLE CANCIONIST CONCOUNTED TACABITABLE	180
40		
	GATCAACTTA GAACTGGTAC GGACAAGGG AATCTGACTG TCTAATTAAA ACATAGCATT	240
	COGATECTICA GARACTICATE TIGACOCART GIGATTICIG COCACTECTIC TGARTETCAR	300
45	desired districts desired templetic templetic	300
	AGTGAAGAAA TTCAACCAAG OGCOGGTAAA OGGOGGGGGT AACTATGACT CTCTTAAGGT	360
	ASIGNAMA TICARCOMS COCCOSTANA COCCOCARST ANDIMICACT CICHIANGGI	360
50	ACCCAPATICC CTCGTCATCT AATTAGTGAC COCCATGAAT GGATTAACGA GAITCCCACT	420
	GTCCCTATCT ACTATCTACC GAAACCACAG CCAAGGGAAC GOGCTTGGCA GAATCAGGGG	480
55	CCAAACAACA CCCTGTTCAG CTTGACTCTA GTTTGACATT GTCAAGAGAC ATACAAGGTG	540

	THE STATE OF SECONDICA MAINCALIA CUTTATAGE TECHTIACIT	600
5	ATTICAATTAA GCGGAGCTGG AATTICATTTT CCACCTTCTA GCATTEAAAG TOCTATACCG	660
	COCTEATECC CETTEAACAC	680
10	(2) INFORMATION FOR SEQ ID NO:865:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 686 base pairs	
15	(B) TYPE: mucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1544RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:865:	
	GATCTCAACA AGATCAATAG GCATATCCTG CCGCCTAGGG ACACCACTGA ATTITTATGAC	60
35	CACAACCOCC AACACTTCCA COCCACTGTG ACAATCCAAC AAATCCCCAT TCCCATGCCC	120
	AAACOOCOCA AGTOOCTGAT GAAGCACTGC GAGGOCGATG TOCTAGAAGT TOCATCTGGT	180
40	ACTOGTAGGA ATATAGATTA CCTAGACTTG AGCAAAATCG ACACAATCAC CTTTCTGGAT	240
	OCCICTAAGA ATATGATGAA GATCOCCAAT AAGAAGITCA GAGAAAAATA COCACACTTC	300
45	AAACAAGCTG CATTOGTAGT TGGAAAAGCA GAAGATTTAG TGGACCTGGC GACTGGGCAT	360
	TOSCCTCAGE AACAGAATCT GGAATTOGTC AACTCTCCTG AGCAGGTGAT CCCGGAGTCC	420
50	AACCCCAACG TTAAATACGA TACCATCATC GAAGCCTTCG GTCTGTGCTC TCACCATGAT	480
	CCTGTACOGG CATTGAAAAA CTTTGCCAAA TTGCTAAAGC CTGGCGGAAG AATAGTTCTG	540
55	CTTGAGCATG GCAGAGGGAC CTATGACGIT GTGAACAAGA TTCTAGACAA GAGAGCCGAG	600

	CACCUTCICG AGACCIGGGG CIGCAGAIGG AACTIGGATA TIGGCGAAAT TCTAGATGAC	660
5	TCTCATCTAG AATCGTCACC GAAAAA	686
	(2) INFORMATION FOR SEQ ID NO:866;	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 683 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1544UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:866:	
	CATCAAATIC CAATCTCCGT CAGCGTCAGG CAGCCGCGTT ATGTGTTGAA CTCTTCGCTG	60
30	CTTCTCTTCT CTTCGCTGAA CCCGCAAGAA AATTCCACCT CACGCCGAAC CAGAGGCGAA	120
	AAACTGAAAA TGAAATAAGG CGCCGGCTTC CCAGGACGTT GCGGGCTCGT GCAGCTCTAC	180
35	TTGCAATACC CGCAATAGGA CTAOCAGACC TTATTAGACA CTGTAATATG TGGGCAGCAG	240
	TAGGIGCAGI CIACAAACIT TIAIAGOOCA GCCGGGCGIA TIACICITIT CIGCICCCGC	300
40	GTCCGCCATA ACTIGICACT CACACTCCCG CCCACCGAAAC CTCCCCACCCA GTCCCCCAA	360
	TAATGAGTAA TGFTCTATGT ASTGGTTOCT AGGGGGCTGA AGGCTATGCT CTGGGGTAGC	420
45	TOGANTOTICA COCAGANCAT GOOCTTOCTA GOTGOCACTT TOCOCACGAG GTOGANCGAC	480
	AGCOCAGTCA TCCCCAGGAT CTCTCCCCTG CTGTGCATTA TCTCGAGCAC ACCCCGGTGT	540
50	ATGCGGGGT GCAGGTCTGC TGGCGCGGGC TCGGGGCTCGT CGGGGCTGTA TTTCTGGAAA	600
	CAGTGACAGT GGATGTAGGG CAGCACCAAW TGCTGGGTGG GCAGCGGGGT CCTCCGAGAT	660
55		

	CCGTGGCGCG AGTACAGCCC GGC	683
5	(2) INFORMATION FOR SEQ ID NO:867:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 714 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1545RP	
20		
25	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:867:	
	GATCATTAAT CAGCCATCGC ATACCCGGGC AACATGACCA TTAGCTCCTG CTTTCCACAG	60
30	AAACAACOGA CTATOOGTAT AGAACTTGAT GATAGAAGGT TGAGGCATTT AAAAAAGTOG	120
	CTAGACCOCC CTITAGATCC COCTACGACA GACGAGAGCG TCACAGCCCT TGTGAAGCAC	180
35	TATGTACTAC AGGTACTACT AGAGTGOGAC ATCGCAGCTG TGAAGGGCCG AAAGAACGAG	240
	TICTOCCACC ACATCACCCA GTACCTOCCA CGTATCGTCA AGGACCACAG CTGTCTAGAT	300
40	GOGTTGTTTT ATCAGCTAGT GGACTTAGGC GAGCCTCCCC CCCCCAATAG TTGCCCCCCA	360
40	CABCIGOGIG TOCTGAAAAT COCAGOGGAC COCCTTOGCT GOCAAACCTT GOGTOCOCAG	420
45	TITICOCCUTT TIGGAGOGET CACCAGGGGG AGGATTGATT ACGTGCATCG TGAGGCATTC	480
43	TTGCAGIATG CGGATGCCCC CAGCGICGIC CGATGITGIT CGGICCGGAA GOCTITCITG	540
50	COGRACOGGI TOGTICACET COACCOCTICC TOCCCACCOC TOCCAATUAC TAACCOGTICT	600
	CGACGICIGG COCCOGATC ACGAAACAAC TGTGCCCCAG CATGGATCAT CTGGGGTGCC	660
55	TOCCOCCAACT GENERATET TECATOGREE ACCRECACT COCCOCRACA TOTA	714

(2) INFORMATION FOR SEQ ID NO:868:

5	(i) SEQUENCE CHARACTERISTICS:	
3	(A) LENGIH: 576 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1545UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:868:	
	CATCATCTTG CAGGGACCGC WCCACGTGGC GTAGAAGTCC ACGACCACGA GCTTGTCGGA	60
25	GCCCACGGGG GACTCAAATT CAGAAAGGGA CTTGATTTCG GACACCATTG CGTTCTGTGT	120
	CONTROL OF CHANGE CHAINES OF CHAIN	120
	GECTGACTGT ACCTTGTGTA TACGCAGTAC CCAGGAAGCC GGGCGGAGCC CCGCCTTTTA	180
30	TACCCOCCCC CCTGCCGCCA CGTGTCACCA CGTGCCGGGGT CTCCCCTCTA TTTCCGCTCA	240
25	GEAGATAAGG ATGACAAACG CGTCCTCGCG CGGTCCGCAT TGACGTCTTC GACACCAATG	300
35	CAACCTCTCC TATAACCCCT GICTCCCCCC CCACCCTTCT CAATCCTCCC TCTCTCTCT	360
40	COCTITIONET ACCOCAGOOG COOGNITION TACGITICOG ACCOCGITIOG ATCTCCAACG	420
40	CACOGTOGAA TAACGAACAT GAAAGCCAGT TIGTACAGTAG CTACACCCCA GCAGACGAAG	480
45	CATCAGCAGE CAGTTGAGAG CGOGTACGAG AAGTTCOGTT ATAGAGCACA CTCGAGACCA	540
45	TAGAGGICAT COOCTAGGOG GTACTICAGG TCAGGC	576
50	(2) INFORMATION FOR SEQ ID NO:869:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 741 base pairs	
	(B) TYPE: mucleic acid	
55	(C) STRANDEDNESS: single	

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1546RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:869:	
15	GATCTICCIG CTATCCAGAA ATGCGAAGIT CITAGACAAC GCCCAATTAA GCCCCTTTIC	60
	CAATAITTIG AGGGIGGITT CATAGCIGGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT	120
20	CIGITCATGT TOSCTCATGA AAGGIGTOTO TATCAAATCT AGCTOCATCA TOGCAGAGTA	180
	GITATTATCT TICTICCAAG ACAGACGCAC ATGCCGCAAC TTCGTCAGCA TTACAGTAAA	240
25	ATAATOGTAG AACCOCOCAC TCACAGAAGC GACGACOOCT CGAAATGAAG TCCCCCCGTA	300
30	AAAGATOGTG OGGCCCTGCT TCTCTATCAC AAGATGGAAC TGCCAAAGTC TGTTCACGGG	360
	GCACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT COCTCTTCAT	420
35	CCCCCCCACC TCACTCTCAA GCTCCTCCAT CCCTCCCACCA ACCTCCACAT TGCCCGTCCA	480
	CCTGAACACC TCCCGTGAGT TCACGTCGTG CGTAAACTCA GACAGGTACA CACACTGGGG	540
40	CAGGCCCTTC CCAATACATG TAGAGCACTT CGGCCGCCCC TTGTTGCACT TGACGCGCCC	600
	CTTOCOGCAG AACACGCACG ACTTOCTGAC CTTCCGCCTG GTTTTCACAA TCTTGCCATC	660
45	CCACTCTCCC ATCCCCCCAG CTTCAACCAA AATGAGTAGG TCATATTATT TACCTGCTGG	720
	TAATCITGAA TAATGCTCAC T	741
50	(2) INFORMATION FOR SEQ ID NO:870:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 707 base pairs	
55	(B) TYPE: nucleic acid (C) STRANDELNESS: single	
	(C) DANGE THE COLOREST COLORES	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1546UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:870:	
15	CATCGCGGAC TOGAACACIG GCCGGAGATG CGCGGGGCCA TCCTGGTGGT TTCTGCGGAC	60
	COCAAGGACA COCCATOGAC GAGOGETATE CAGCAGACGC TOCACACGTC GGACCTCTTC	120
20	AACCACCCC TOCOCCACGET GETCOCCCCG COCTTACCCCAC ACATGCCCCT COCCCATCCCCC	180
or	COCCECCACT TOCCCACETT TECCCCCCCTC ACCATECAGE ACTOCAACTC GITTCACCCC	240
25	ACCIOCCIOS ACICATITOS OCCEATOTIC TACAIGAACS ACACITOSOS COSCATIGIC	300
30	AACCIGIGIC ATCIGATCAA CGAGTICTAC AACGAGACCA TOGTOGOGTA CACGTTIGAC	360
	GCGGGTCGGA ACGCGGTGGT CTATTACTTG GCGGAGAACG ACGCGGGGCT CTGCGGCTTC	420
35	CTCTCTGCCG TCTTTGGCGC CAACGACGGC TGGGAGACCA CGTTCTCGAC GGAGCAGCGC	480
	GCCACCITOS COCCECAGIT CGACGAGIGO GIGOGOGGCA AGCTIGOGAC GGACCITGGAC	540
40	GACGAGITGC ACAGAAGAGI TGCCCGCCCIC ATCTTCACGA AGGICGGCCC AGGGCCCCAA	600
	GACACTAAAT CCTCGCTCAT CGACCCGAGA CGGGCCTGCC CGCTGACGCT ATTCTCCTGC	660
45	TATTITCIGC TCTGTATACC CTGCCAGACC GCGCTATATA TATAGAA	707
	(2) INFORMATION FOR SEQ ID NO:871:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) MODOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1547RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:871:	
	GATCCTCCGC CTACACCAGA ATATTICTGG CCAATTAGTT GTTCACCATC GCCCCGAACG	60
15	THOSHGAMOC CACOGOCCATA COCTOCCATG COGAGTOCAA THTTTCTTOG OCTGACCTTA	120
	AATTGTTOOG TCATCATGAG TATCOCATCA TGTOCATTCA ACTCATCAAA GITGTCAATA	180
20	CCCATATCIT CATACCGACG CPTATCTAGG TOCCATTTGT ACCCCGAATT CGTAGCATTG	240
25	TACAAGITIGU TATIGGITAGCC TIGTTCGCTCT GACCATGCAC CGTGGTAGTC GTATIGTCATC	300
20	ATATICCACA TOCTGAGATA CTTGITCATC TCCTCAACCG GGAAAATGCC AAGTGTCTGA	360
30	CCAAAGGCCC GTCCTCCCAT CCTTAAGTCG AAGCGCCGTT CTGTAGTCCC CCCGCGCCCC	420
	CAGATATTGT CPTCCAATTC GICCATCTTG TGTCGCAAGC GGCTACACAT TTCTAGATAC	480
35	ATCTGGGGTT CGTAGCCATC ATCCTTAGGG AACTCCCAGT CAAGATCTAT CCCATCCAAG	540
	COGTACTOAA ACATTGOGIC GATOGOGAG TOGATGAAGT TGTTAAACTT CICCIOGTCA	600
40	COCACAATIT TATGGAACOG CTCCCGATTG GAACAGCGGC CAACGGCCAT CATGAGCTTG	660
	AAATCOGTCC CTGGCCGCGT CTTGAGGTAA TTAAGCTTCG CCTATTGCCC	710
45	(2) INFORMATION FOR SEQ ID NO:872:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 608 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55		

(vi) ORIGINAL SOURCE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1548RP

	(A) ORGANISM: PAG1547UP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:872:	
10	GATCTCTGAG GGTTCCAAGG CAAGCCCGCC GGAGCTTGCC CAAATTGTGT CACCCGCTCT	60
15	CGAGTAGATG GTOSCCTTGT CGACCTTCCC GGTTGCTAAC AAGTTGTCAG TGTAGGCTAA	120
	AGCTCTAGTT AGTACCCACG AACGGGCCAC GAGCAGAACA CGTAAAAACA CATACCTTGC	180
20	CAAGACATGA TGCGITCCGG ATGAAATCTG AGTTAGTGCT AACACTCGCA GATGCTCTGG	240
	TGAGTGGAAT CTACGTATCA ATAGTATTGA TTTGTCAATA AATATACCTT GCCTTTTTGT	300
25	AATCTTTTTA TATAAGGGT TOOGATCTOC TGACATCATA GCACAGGAAT TAAGTATOOG	360
	COTIAACCAAC TOCCCOCCTA ATCCCCCCCACA CACCCCAACT CCCCCCTIAAC CCCATCCACA	420
30	TACCGCAGAG ATGCACTGGC GGCTACATAC TGTACACAGG CTCGCAGCTA CTCGTCGTCT	480
	CACTOGAGAA CAGOCACOTT GOCACGOTTIC ACAGOGACCT CTTCATCTICC GOGOGGGGCC	540
35	GEOGGEGEAG CAGOGTACTT GEOTIGOSCOC TOSOGTITICA GCTGCTGCAG ACGOGGEGE	600
	TTTAGGIC	608
40	(2) INFORMATION FOR SEQ ID NO:873:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
45	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	

1129

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:873:	
5	GATCATCATT OCTOOGITAG CGATTOCCOC CAATTITTACA OCTOGTTCAT COCTAGOCOG	60
	TAACOCCACC GOOGSTAGIT TOCTGTOCTA COOGTCOGTG GIGITTOGTT TIGCATOGOG	120
10	ATOSACAACA TATOCTOCAG ACTACACTOT CPACATOCCC AAAAATTCTA ACAAATACCG	180
	CATCHITTIC TICATGATIC COSSICTION GACCOCCHIC CIGITOACGI TGATICHIOS	240
15	ACCIOCIOCO COCCOCTETE TOCACACAAA TCCTACGTOG COCCAATATT ACAAAAAACA	300
	TICCGIGGGA GGICTGIGCT TIGCTATACT GGCIGAAAAC GCICIGGGGG GGITIGGGCA	360
20	GITCTOCTOC GITGTACTOG CCATGTCCAC AGITGCAAAC AATATTCCAA ACATGTATTC	420
	CATCGCTCTC AGCACCCAGE COCTGTGCAG TCGTTTCGCC CGTGTGCCAC GAGTGTTCTC	480
25	GACCCIGGIC GCCAACGCAT GCAGCIIGGI CAITGCAATC GITGCGIACT ACAAGITTIGA	540
	GACCITCATG ACCAGCTITA TOGATICAAT TOGCTACTAC CICICCATAT ACATOGIAAT	600
30	ATCIGICACT CACCACTICG TCTTCCGCAA GOCCTTCCGT GGTTACACGT CAGCCACTGG	660
	GAACGICCCC ATCITICCICC ACCITOGITIAC GCIGGCIGCC CIGCCC	706
35	(2) INFORMATION FOR SEQ ID NO:874:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGIH: 590 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1548UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:874:

	GATCCACAGA TIACAGTITAC AAGCCAGAGT TOGGCCTATT TAAGGAACAG AACCTATACC	60
5	ACATTICAAG CICCACTITI GOCACOCCAA GACCGATTIG COGATTAAGI ATCTIGAAGI	120
	THECACTUAG ACTUAAGAAC TACTATTACG ATACTATAAC AAAGACGATG ACTAGCACAG	180
0	COGACCACAA GCAGCCCATT TOGTTGAAGG TTAACGGGGC TCTATTOGAC GTOGAGGGGA	240
	CCATCATCAT CICCCACCCC GOSCTADCOG CCTTCTOGAG GCAGTTTGGC AAGGACAAGC	300
15	CGTACTICGA TECCSCACCAT GICATCAGIG CCACCCACGG CTGGAGAACC TACGACGCCA	360
	TOSCIACCTI COCCCAGAC TATCTGAGTG AGGAGTACCT GACGAGACTG GAGGGCAAA	420
20	TOCCAGACAA GTACGOCAAG TTCTCCCGTCC AGGTTCCCCGG CGCTGTTACG CTCTGCAATT	480
	GCCTTGAACR AACTTCCGAA GCAAAATTGG GCCGTTGGTA CTTCCGGCCC CTTCCACATG	540
?5	SCACCANGIG GITOGAIGIC CICOSCAICA AGOGICCIAG CACCITCAIT	590
	(2) INFORMATION FOR SEQ ID NO:875:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 736 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40 45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1549RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:875:	
50	CATCHOCTEG GEORGACCAC CGAAACCCGA CEGCTTACGG TCATATCTEC TCTTACCCEG	60
	ASCARACARG GRASCOTTAC COSCOTTIGITA CTIGGGTICACC TTIGTIGCTIGGG TIGTIGCTTIGGG	120
55	GCAGGCCTTG COCTTGCAGT AAGTCTTTCT GGTCTTTGGA ACGTTAACTG CACACGTTAG	180

	TATACCICLY CYTCLCLAST COCTYTTOGA TOTOCASCOG COCCGTCAGA AGGCCCTGCT	240
5	GTAPOGAPOC GTGGCCCCCT GGCGGCGCTC CGCGCTTCCC CTCCGTCATA TTGAACATAC	300
	CCATTOUGAG AAGTACCTTC TGTGATGCTC TGTGCTTACT ATCAAGCAGG ATGACACCGG	360
10	COCTICAATC CIGAAATITA CCATGITIIT COCTICOCCA CCTCOCCCC CCCCCCCCC	420
	COCCOCATT CACCOCACA	480
15	ACCACGCAGC GIGGIGATIGC ACCCATGIGC ACTIVICITIES GGIGTICAAT AAATACATGT	540
	ATGOGTGTAG TCACATGITT GTCACAGGCA CTCCTCCCGC GCTAACGCCT CCACATTCCC	600
20	CAATGOSTGT GGCGGCATAG GCCATGGCCTTG AGCTCTGCGC GCGGTTAGAG	660
	CCCAAGTCAT TAGACTGCGG CACTGCAAGC GTCTGACGGG CAGGTTTTAA GCTGGTGTGT	720
25	GGCCIGCGC TACGIT	736
	(2) INFORMATION FOR SEQ ID NO:876:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 707 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1549UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:876:	
50	GATOCATGIA TAATCACOCC ACAGCACCIT TIGCAGGIIC TOGCGCTIGG CCCCCAGCIT	60
	CTGCTCGTAG AACTTCGCAA ACAGACTGAC GTTGAACCCC CACCCATCTG CAGGAGAGC	120
55	AAAAATCACA TIGITCOGGG ACGGGTOGAA GIATAIGIOC GCATCATOOC GCTOCACATA	180

	CTGGGCTGG GCGTCCTGCT CCAGTTTCTC TCTCCAGGAG AGGTCATCCA GCAGCGGTC	240
5	CCCCCCAAAG AAGGACCCCA GTACAGAGTT GACCTGTTCA ATCGTCTTCG ATAGATCCAC	300
	GTAGGCCTCC TGTCCCGTCA GCTGGAGCTC CGTGATCAGC CGATGGATCT TGTTCAGCAC	360
10	CAGCATTIGGT CTCAGCTTCT COGTOCAGCA CTGCCGCCAGC ACCGTAATCG TCTGCGAACA	420
	CACACCCTCG ACCACGTCCA CCAGCACGAT COCCCCATCA CATAGCCGCG ACGCCGCCT	480
15	AACCTCOCTG GAGAAGTCTA TGTGGCCCCG AGAGTCGATC AGGTTGATTA AATGTTCGTT	540
	CACCACCOCC TOSCIOCIOC COTOCIGITI GIGAACCACT COGAAGITAC AGAGAAATOG	600
20	CACTECACTC CATCOTGATG CCTCGCAGCT GCTCATCTGG CCGCGAGTCT AGGAATCGCA	660
	CTTTCCCCCC TAACCCCTGT GAGATAATAC CGTTGGATGC GAGGAGG	707
25	(2) INFORMATION FOR SEQ ID NO:877:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1550RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:877:	
45	GATOGAGIAC ACAAAGIACA TOGATOCIOC CAAIAACIAT AGICIGAAAT CAATOGGITC	60
	CITAGOGAAT GCAGATGAGT TOGOGCAGCT GGCATCATTT AACTOCATCA GCCATTATTT	120
50	ATTOCCTORA TOCCOCATOTO TOCCAGRICACT ACARTTUTA TIRACCTORT CIARATTOTA	180
55	CCCAAAATTA ACGAAGGAGA ATCAAGAATC TOCAATTATC GAAACACTGC TGTCTCTCAG	240

	TGAATTTACS TIGCIGCACG ACTICICICT CCAGGCAGGI TICCAGGIOG AAAAATCGGI	300
5	CATTITICAAG TACTITITOOC GCTTTITICAA CAGCOCACCA AATGOGTICCA GGGGACCGGC	360
	CAGAAATGAC AAAGGCGAGG AACAATCTTC GCTTACTGCC CAAAAAGGAC TATTATTATC	420
10	THEAGACHET TETHGATGHE GEAGACHEET TOSCAAAGHA THEOCHAAGE TACTCAGGHG	480
	GACAACCCTT CAGACCATCG CATATATTGG ATCTCAAAGA TGATCCATTC AGAATCATAA	540
15	GCAAACTGCT AGAAACGAAT CCCAGTCTGT ACCGTGACGT TGAAACGACT TTCGAAATCC	600
	TCAAGCAATT ATATGAAGGA TIGCAACTGC AGCCTCATGA TCCAAAGTAC ACAAGTGAAT	660
20	ATACCCGTTT GCTAGTCTGT CACATTGATT GTGCATTGGC AAATAT	706
	(2) INFORMATION FOR SEQ ID NO:878:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 736 base pairs (B) TYPE: nucleic acid	
30	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1550UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:878:	
45	GATCTCCTCC COCGATATCA TGTCTAGCCA GGATTCCAGG TGTTCAGTAT COCTCATGTG	60
	TOCCOGFITTA CITICAATCCA TCCATTCTOC COCAGCCATG ATATACTTOG COCGATACCC	120
50	AAACCCCAAA TOCCOCAGIG CGICCTCCCT ACCCCCTTCC ATCACCTCCT TOCTCGTGGG	180
	CAATGAGTAG TATGGAGTAC CGTCGAGCTC GCCCAGGAAG CTCCCGTACT GCCAACACAG	240
55	TOCATOOCAC ATCTTOCTICA TOCOCCCCAT ATTGTTGTTG CTAGACCAAA TAAACGAGCA	300

	CAGIGICIOC CAGGITICCT GICGCAGIAT TOGCACOCCA CGAIGIGITT TOCCGAIGAA	360
5	ACGIGIGICT OCTITICIOCC ATTOTOCTAA CAAACCCTCT AGGITCACCT CCATCCGTAG	420
	GTAGCOCATC AGCCATTGTC GTGCCCCCC GCTGCAGTCG TCATCTTTAT TCCCAGCTAC	480
10	OCTGAATTCA ATACTGCACT GATOGGGCTG CTTCAATACA ATAATACGAT AGCCCAGCTT	540
	GICATTIAGI AGCATGCICG COGAATAGIA CCITITCICA IGATTCCAGA ICCACCIGAA	600
15	COCTTGACCA CATTOCAATA CATGGTCCAG GACTATTTCT CCCTTTGGGA ATATCAATCT	660
	GITAAACTIC ATAACTGICG ATACAGCACT GACCTCGCTC TAATAATCAG CGTCACGGCG	720
20	CIGCTICGAG CATGIT	736
	(2) INFORMATION FOR SEQ ID NO:879:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 702 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1551RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:879:	
45	CATCTCACGT CAATCGCATA TCTCCTCAAC CCCCAATTCT CGTATATTCT CACCACATCT	60
	TOGOGTICANT TACGTOCACT TTGGCCGAAG CCTTCGCACG AGCTTCTACG ATACAGAATG	120
50	CTGCCAGGTG CATCITAAAA AGCGGGTTTA CAGTGAGCCC TCCGTCCTTC AGGGCACCAG	180
	CCCCTAACTG TACATAGITT CTGTTATGTA GTTTGCCTTT CCTCGCGATG CCTGCCTCTT	240
55	CTGCAACAAA AACAGGCGGT AGAAGGAAAT TCCCGTIGOGT CATCGGTIATC GGAGGGGGTC	300

	TOCCIOGATO TOCOGRAGIAG CITTATIGAGO CATTAGTICAG GRACOCOGAT TITOGAGGACA	360
5	GATTTAGTCT TTTCTGTGTT CCTCCAAACA GOCTTGGAAT GTATCAGCOC GCTGOCCCAG	420
	CGACAGGCGA CACCGCTTCA CATAGGGAGA GGCCACCCAC TGAACACGGG GTGCACTGTC	480
10	AGGGGGGGCA GCGTACTGCC TACAATGGTA TCGTCCGCAA ACGGCAGGCC AACCGGCAGA	540
	GCGGGCATTT AGATCTAAAT TTATCAGCCC ATGGACGGAT GGATTTACGG CAGCGTGTCG	600
15	CCGCAGCACG GGGCACGCCA GACTGCCAGG TGGCAAATAA TTCACATAGC AACCTGCATT	660
	ATAAACATCC CAAGTCATTA AACTTACTAA ATATTGTTGC GT	702
20	(2) INFORMATION FOR SEQ ID NO:880:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 735 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1551UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:880:	
	CATCCCCCCC AACCTGCGCA ACTGCACGGT GCGCTACGAG GACCCGGGGG GCGCAGTGCA	60
45	GCTG9000CAC TACCACTACT CCACGCCACCT CCACGCCTAT CTCAAGCATA TOCACGTGCA	120
	GTACGAGGIG CTGGCGTACA ACTGGCCGAC GTTTCTGGCG TACGTGCAAG AGCTGGAGGA	180
50	COCCEACTIC COCCEACTICT TOTOCCACT COTOCCCTAC COCCCCACA ACCEACCTGTA	240
	COCCOCCAAG CTGTGCOCCC GGCTCGTGAA GGAGCCCTCG ATGCAGCAGC TGATCACCCC	300

	TOCADCACCA CIGODACAGO AAGOICGACG AGCOCGACG CIICCIGCOG CIGCOGAGCA	420
5	ACCTRICTICC CAACRITICS AAGAAGACTA ACCARCICCT GTGGACGGTG CTGTGGGACC	480
	OCTITICCAGAG CGACGCTAAG ATOGAGAAGA TOCGGCCCCG CAACGAGGCC GCCACGCCCG	540
10	ACCOCCCCC CEACCACCTC CTGACCCCC COCACCCTTA COCCCTGAG CACCCCACC	600
	OCTITACITAG COCCIGIOST CACIGIOSCE GACCOSCOC COCCAGGO OCTIGACATIC	660
15	AACGAGCTTC COGATGAATA CTGCATCACC AAGACTGACT TOGACOGGCT CGCTAGCCAC	720
	GOCATCCCCCC TCCAC	735
20	(2) INFORMATION FOR SEQ ID NO:881:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 804 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) CRCANISM: PAG1552RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:881:	
	GATOGTOGGO TOATGOCACO ACAACTTOCA OGTOCACTGO ATCTACOAGT GOCTOAACAC	60
45	CTOCACGICC AAGGGCCICT GTCCCATGTG CAGCCAAGGC TTTTCACTCC GGGAGGCCAT	120
	COGCATTAAC GAGCCCCACC GCGACAAGTT CGAGAAGGTG TTGATGAAGG CGCGCCAGCA	180
50	GAGGETGETG AGGETGGCGG GGGCCAACGC GGTGGGGCGG GACCAGGACG ACGTCATCAT	240
	CKACCAGGAG TICATCCGCT GACACTAACT AGCCTGTGTA CCCATGTAAA AATAATGCTT	300
55	CCAACCAGAT TOGAACTGAT GATCTCCACA TTACTAGTGT GGCGCCTTAC CAACTTGGCC	360

	ATAGAAGCAA TACGAGOGIC TAGCGGACTG COCCGGGCTA TATGCGCCGG GCGTGACCCC	420
5	GACGAAACGC TOGOGOCCAA ATACCTGATC CCAGGITTOC AACGCTGGTC ACOCAACTTC	480
	TOCCACGIGC ACIGCACACC ACGCCAGCAC TATATAGGCC CGCACCCGCC AGGCGITICTT	540
10	GOCAGGTCAC CGCGTCCAGC TGTGCTGGCA GCATTCCACC TGAAAAAGTT TCACCAGCAG	600
	ANAGACTITIT CCACTICICA ATAGCACTIC TATCCCCTAT TICCTCAGCA GITTTGCAAT	660
15	GAGCTACACT ACCAGACAGA TIGGAGCTAA GAACACCTIG GACTACCGGG TGTTCATCGA	720
	GAAGOCOOCA AGGICOICIC GCCGITCCAC GACATCCCAT TGTACGCOGA NGAGAGAACC	780
20	AATCTTCVAC ATGGTGGTGG ANAT	804
	(2) INFORMATION FOR SEQ ID NO:882:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 490 base pairs	
	(B) TYPE: nucleic acid (C) STRANDETNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1552UP	
	(-1, -1, -1, -1, -1, -1, -1, -1, -1, -1,	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:882:	
45	CATCHTOCAG ACACOCCTOC GOOCGIAGIC CGTOCCAGTG CAGACTGCGT CGCCGAATAA	60
	ATACCTTICT CCCAGGCGT CGCCCAGGCG TTGCCGGCACT CACCGCATAA AAGAAACACG	120
50	CTGCGGCCGC GCGCCCCAA AGCAGCCAGG CGCAACGGGC GCGCCGCAAA AGCAACGGTG	180
	ACACACGATA TOGCACATTC ACRITACATAT TATACATAGC COGCCGCGCC ACGCGGCTCA	240
5 <i>5</i>	GCCGCCCAAG CCGTACAATG TGCCGCCCTIG GCCCTTGACC GCCTACACCA CGTCGACCGA	300

	GETGACGETC TTGCCCTTGG CGTGCTCGGT GTAGGTGACG GCGTCGCGGA TGACGGACTC	360
5	CAGGAACGAC TIGAGCACCG CGCGCACGIC CTOGTAGATG AGGCCGGAGA TGCGCTIGAC	420
	OCCOCCACOS COCOCCACOS GOCOCATOOS GOOCTTOGTIC ATOCCCCTOGA TGTTGTCCCC	480
10	GAGGATCTTG	490
	(2) INFORMATION FOR SEQ ID NO:883:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 691 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genemic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1553RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:883:	
35	GATCCOCAGG TOGTACACGT TCACAAACTG GTCCGGGTAC ATCATGTTGA ATCGCTTCGA	60
	CTTCCCCCCC CTCACCAGCC TGTGGTCGCG CAAATCCATC GAGCTGACCA TGCACGAGTG	120
40	COCCEAGAAC GICTICACCA CCGIGITICCT GITTIGGGTCC ASCAGGICGA GCATCCCGIT	180
	CTGCCCCCCA ACCCCCATCA GTCCGTTGCT CGACTGCATC AGCTTCACCT TCGACGAGTA	240
45	CTGCACGGTG TTGCTCAACC GCCCCTTCAC CAGGTCCACC GCCACCAGCC CACTGGCCAG	300
	GITGGICCCC COGCAGIACA COGIGITICIG CGAGITIGCIG COGIAGCACA TOGCCCGCAT	360
50	GTCGCATAGT TGTGCGATGT CCGCCGACGT TACGTGCAGT TTCGTCACGC TGCGCCCGTT	420
	COCCANGTIC ANTOACTOCC COCCCAGOCA CANGACOCCC TOCTTOTOCC TCAGCAACTC	480
55	CACCACCICC TCTGCCCCCA TGTGTCCCCT GTCCCCCCTG TATACCCACT ATCACCGCTC	540

	GIALGALGAL ALCOGICCGI AIGIGICCCC ACCCAGATCA GATTGACGIC CTGGTCAAAC	600
5	SCCATCTICG TOSCOCICIT CTCCTTOSCC TOGTAACCCC AATACAACIT GOOCAGGTGC	660
	TOUTIGNOCT COACCOOCGA CTOUTATIGNA A	691
10	(2) INFORMATION FOR SEQ ID NO:884:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 708 base pairs	
15	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1553UP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:884:	
	GATCCGCCCT GTGTGCCCCCC ACGCAATGCC TACCTGTTCA CCTGTCTCCA GGCTGCACAC	60
35	COGAATOGAG COGTCATCCG ASCATGATOC AACCAGTOSC COGTCGTOSC TCACCACCCC	120
	GCAGAAGATC GAGCCCTCGT GGCCCTCCAG CCGCTGCAGC ACCGCCCCCG TGTGCAGCTC	180
40	CCACACCACC ACCOCCCCA TCACCGTCCC CCCCCACACA TACACCCCAT CCCCCACCAC	240
	CTTCACCGAC COCCAGTACA GCACCGACCG CTCACCCGCG TTCATCCTGC GCACCACACG	300
45	CATCTCCAGG TCCATCTCCA GCACGCTGTT GTAGCACGTC AGCAGGTAAC ACGAGCGCCC	360
	GTCCCCCCTG AACGCCCCCC CCACCACCCA CTCCCCCCTC ATGTACTCCTT CATACTTCAG	420
50	GITCCGCCGC GICATCACGT CCTCCAACTC CAACATGCTC ACCCACCGGT CCCCATATGC	480
	AATTACCCAC CCCTCCTGCA CGCATATCCC GTGCACCTTG TTTCGCTGGA AAACCCGGCA	540
55	COCCITICACE ACCACTOCOC COCCATACTE GIATACCIAS ATTICCOCCO COCACCETOC	600

	TAGGCACCTC COGTCCCCGA GAATCCGCAC TGCAGTGCAT GGCGCAATGT CATTGACCTT	660
5	ATCCAGCGAC ATATTCATOG TTTAATCGAC TATGATCCCG ATCTAATG	708
	(2) INFORMATION FOR SEQ ID NO:885:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1554RP	
	(A) CONTROL EMELOPITE	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:885:	
30	GATCAAACTA GGAATTTTGT ATAATACTGA AGAAGGTCCC ATATTCAAGT CTCTATCCAG	60
	CGATGATGAG GAAGTGGGTG AGATTGTGCT GCACGACCTG ATGAACAATC TCGATTTCAT	120
35	AACTATOGAT CATOCTGACA GATOGAGAAA OCAAACTCAT CAAGATAGAC CGATGATGAT	180
	CAAGAACTAG TITGAGATCC CTCTGCTACA AACACATACC TAGAITTCTC ATATTITATA	240
40	CIGAATACAT ATAATATATC ATTTAACTGT CTTCATTCAT GAGACGTCGT CTAAGTTCTG	300
	TECTECTICAA CITETTITTIC CACTIGICAG CCTCTTCGCC CCCCAGTACG TTCACCACAT	360
45	SCACSSCTAG CTTCCTCATT CCTTTSCTCT CACSCGTATC GITGATTGTC TGSSCACCGG	420
	CCACAGITTC CTCACTCACT ACCAGGGCTT CGATACCAGG TTCGCTACCC GTGGGCCCGC	480
50	ACACGICITG TAACGCAAAT AITTIGAITT CCAGCCCCCG TITCAGCCTG TGAAGCAAGC	540
	TOCACACOTT ATCOCATCOT TOSTCGAAGG ACTGAAGCTG CTCCCTGTAT TTCTTGTTCC	600
5 <i>5</i>	GCAGCAGTTC TTCATCTGTA ATCCCCACGA TCAGCCGGGA AGCAGTCAGG AGCGCGGCAA	660

	CACTGAGCAA TATTTTATGT COGTOGTGTA AGTGGTOGAA AGTGC	705
5	(2) INFORMATION FOR SEQ ID NO:886:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 727 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1554UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:886:	
	CATCACTGAG CAAATCAAAA CCTTGAGCAG CTTCCCTGTG TTGCGGTTGT ACGGTGTGA	60
30	CTGTGCCCAA GTTGAGACTG TCCTCCAGGC CAAGGCTCCA GGCCAAAAGC TCTTCCTAGG	120
	TATCTTCTTC GTOCACCAAA TTGAGGCCGG CGTGAAGGCC ATCAAGGAGG CTGTTCAGAA	180
35	SCATSCATCC TSSCACGACA TCCACACCAT TTCTATOGGT AACCAACTTG TGAACAACGG	240
	CCAGGCGACC GTGGACCAGA TGGCTGGTTA CATGAAAACT GGCCGCAAGT GCCTGGCTGA	300
40	GCCCGCTAC AACGCCCCAG TIGITICCCGT GCACACTITIC ATCCCTGTAA TCAACAACCC	360
	TEGICIATET GACCIATCAG ACTACATESC TETCAACOOC CACCCATACT TOGACITCCA	420
45	CACTICIOCT GCTATGOCGG GCCCTTGGGT TTTGCACCAG ATGCAGAGAG TCTGGAGGGC	480
	CTOCAACOGT AACAAGAAAG TIGICATCAC CGAGACCOOC TGGCCTACTC AGGGTCAGAC	540
50	TTACOGCAAG GCCATTCCAT CCAAAGCCAA CCAGAAGATG GCCTTGGAAT CTATCAGGGC	600
	CACTIGIGGT GATAGOGCTA TOCTATITIAC TOCTITIOGAC GACTACTOGA AGOCAGATOG	660
55	GCCCTACOGT GTCGAGAAGT TCTGCGGTAT GCTATAAGTT GCCGTGTGCT TCTTTATGAC	720

	CIGICIC	727
5	(2) INFORMATION FOR SEQ ID NO:887:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 712 base pairs	
10	(B) TYPE: nucleic acid	
10	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLFCULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1555RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:887	
25	CATCATACAC OCATTOCAOG TATACATTAT AGIOCTCATA ATTATOGCAT TOCAAATACA	60
	ATGGGGCCCT TACCGTAGTA CIGICITGGT AATGCACCGA CGCTCAGGCT TAACAAGCIT	120
30	TITIGITICIOC GIGIATTACT AACAAAATAA TITICCIOCAG CACAGGGAGI AGAGAIGAAT	180
35	TACATAATOC ATATOGACAC CTOGTCACCT TOCAGOGACA TTAACATTTC CTTATGAATG	240
35	CCCAATAATG GIGCCTAAAT CATGIGCTTG GIGIAATGCG CATTATAAAA TGIATGIGCA	300
40	TTATATATTG TTTGTAGCAT CTAGTAAAAC CATGGTAGCG AGGTCTTTGG CCATACCCTT	360
40	CTGAAGAGA ACATAGCAAC AGTGTCTTGT GCAGACAGTC TGCCGTCGAA TGTTGCCTTG	420
45	ANGTANCCAT GAGTACCAAG ACTICTOCTTA ATGANGCCAG AGOGTCCAGA TYTOGTGAAT	480
45	AGTGGGATOG ACTTGAACCA CTCGACATCT TCTGGCCTAA AGAACATATA GCGCACTGTG	540
50	ACGACGOGCT TGTGGAACTT GAATGGATGG GCAGTTAATA TGATTCTCTT GGCCAATATC	600
-	CGIGIGIGGI CTOCGTTCAG GAACGIGCCG TGGCCCACGA ACGICAGGCC CITTGGATCA	660
5.5	CAACCUTTIT CITTCAACTA CATCCCCCCC CACTCCCCACCCC AA	712

	(2) INFORMATION FOR SEQ ID NO:888:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 689 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1555UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:888;	
25	GATCIGOGAA ACAAGCATTC CAACCTAGIT GGAATGGCTG GCAATTAGCA GCTGCGGCAA	60
	GOCAGATAAA GCTAACTGTG GCATAGTTTC CGTCAGTTTT GATTCGGTTT CTCAAGCAGG	120
30	AATACTTIGC TGGCCGCCAC GGNCGCGGTT TTTATACTGT CAGGCCAGCC CGCGGCCTGC	180
	COGGIPATOC CIGGCAGACC COCTCIAGOG CACOCCGAAT COCCCGICAC AACOCCIGCC	240
35	GOCGCAACAT GAGCACCTAA AGGGCCGGCA GOCTCOGCTA GACAACCTGA TGGTAACGTC	300
	GIATIGIAAT ACTTAACTTA TACAGOGITT ATTGATTATA THACTCAGAA ACTGCCGTGA	360
40 45	GACCCACAGE COSCOCCGG AATTGTGTAC AGTAGGGGGC AGCGGGGCGC CCGCCGCTCT	420
	TAACOGTACT TGTOGAAACC AATGTOGTIG GCCTTCTCTC TGAAGCACTG ACGGCAGATG	480
	TTCAAGCCGT ACTITICTGAT CAAACCAGAG TGCGAAGCGC ACACGCGGCA CTGGCGGCAG	540
50	CCCTTACOGT AGITTCTTGG GTGGGAGAAC CAAACGTTTT CGTGAGCCAT CTTGTCTGCA	600
	ATGCGTTAGT ACTCTGTCTG ACCGCTTGGA AACGCTCCGG CCCTCGTTGA CCTCCCCACA	660
	COCIOGRATIC CICATIOCC	689
55	(2) INFORMATION FOR SEQ ID NO:889:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 700 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1556RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:889:	
	CATCAACCAG TOOOCCGAGT CCTATACGAC OGGCATCACG CTGGTGTTOG AACTTCTOGG	60
25	TGACCCTCCG ACGTACCTGC CTAAGGATAG TTTGCCCGCCA GAACACCCTG ATGAGGGCTT	120
	CACGAGIGCT TCIGCGICCG AGCTGCAGCG COGCTTIGCA TICAAGTGIC AAAATCCACG	180
30	AGTICACCCTIC GTAAATGACT TCACGGTAGA CGTATACCCG GOCTICAACCT TOCAGCTGCT	240
	CAATGATAAT ATCTOCTTGT GTTTTGATAT TCTGAGAAGG CAGAAGTGGT GGCACACCGT	300
35	CTEATATOCT ATTICCCAAC TITIGCTGCA TCAAGGCCAG GATTCTGCGG TAGGAGACGC	360
	COCAGCACCC GCAGCOCAAC CCCCGCTCCA CCGCCGCCGA TCAAGCAACA AGGGCTGTCG	420
40	COGAGCAAGT GCGGCCGAGT CAGCCACGCT AGGGGGACGAA AATATGCACC AACTTACCTT	480
	AACGGAAATT ATGAACAAGT CTGTGATTCC CGAAGATGAC CGATGATGGA TGACCGCATT	540
45	GACCICIAIG TIAACGAGAA CIACGICIAI CIGOGGACCA GGAGGGITGC AGCITICIAIA	600
	ACCATCOGAT TGAGAGGTGG GAGGCGTTTG TAGAGTCACT AAGACAGATG CTTACGTAGG	660
50	TATATAATIC TCATCTCACG CCIGGIATGT ATGCGCTIGT	700
	(2) INFORMATION FOR SEQ ID NO:890:	
55	(i) SEQUENCE CHARACTERISTICS:	

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
,,	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1556UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:890:	
20	CATOCCAATA ACGTOCACAT AAGGGAGAGA CTAGAGGCTT TGACTGCCCA GCTAGCCAAC	60
	CCAGGGGCCC AGCAGCCTCA GCAGCAGCCT CAACAGCAAC AGATGCAACA GCCTAGAGGG	120
25	CCASCACCCA TRATGITOCA GCCAACATTG CAGCAGCAAG ACCAAACAAA TCCGTTGAAT	180
	AACAAACCIG CGITCTACOG GICCTCTCCC CACGGAGTTG CGGTTGCCGG AACAGAGTCC	240
30	OCAGOCCACA CACCAATGTC AGGACGGCCT CAGCCGTTGC AGCAGTTGAA CAATAACGGA	300
	AGTATOCTOG AACCGTCATT GTTGCCGCAA AAGAGGCCTA TGCAGGGTGG AATGGATACA	360
35	TIGGIAAAIG CCAITICOCA GCAGGAGIIG CAGCAACAIC AGAAGAAACA TATGCCITCI	420
	CAGAACCATC CTAGTTTUGC CCTGGCTACA GGACAGCCGC AGCAGTTACC ACCGGATGCC	480
40	GCTCCCATAA TACCCCCCCA AAAGAAAGGT GCCCCTCTCC CCCAGTTTCA GAAAACTGAA	540
45	CCAGAGCATG COGCAAAAAG ACTGAAGCAC GAGCAGAATA ACGITTIAAGA GCAACCOGTIC	600
4 5	COGICICGAA TATACCTICG ATTACCCACC CASCTICCAT GCAACATICT GGICCGGGAG	660
50	ATCAGAATCA CATICIATOT GOOCCTTCAG TCCACGCAAC CCACGIGITA CTCCGGTA	718
50	(2) INFORMATION FOR SEQ ID NO:891:	
	(i) SPQUENCE CHARACTERISTICS:	
<i>5</i> 5	(A) LENGIH: 720 base pairs (B) TYPE: nucleic acid	
	(a) The mentale and	

(A) LENGTH: 718 base pairs

	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1557RP	
15	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:891:	
	CATCACCCCA CACATTCCCT ACAAATATCA ATTGCTTCCA CACCACATCT GTCTCCTGCT	60
20	CATIGINGAG AACCUCCAG ATATAATIGI CCAAAGIGAA CTCGICTTIT IGAGAAAACA	120
	COCTITICATA CACACCOTICE CACTITITOGG CTAGACCATA AGCAAGGICT ATAACTICOG	180
25	TGGCAGTATA ATTCCAGACC GGCGGTGGTT GCGGCGGGAC AAGGGACTCC CAGTACCCAA	240
	GTAAATCCTT CGTCATTGAG CTTTTTTAAC ACAGAGCCAA CTAAGATCGA CATGGTAAAC	300
30	GACGCCATTA MITTTGTACC ATTTTTATAG GACACCAGAT ACATTTACAG AAGCACCAAC	360
	COCAATOGIT TIAATOGGIG CAATCAGIGC CATTCITOCA GCTGGGTCCA AACTCTAGAT	420
35	TTACAAACCC CGCACGAATT AGCTAGTGTT GAACCAGCGA ACATGTAAGG AGTTTCATTT	480
	CCCCACACTA TIGAAAACTA CIGCGGIGAA CGCAGGIGGG GCCGCATTAA CGCCATATAA	540
40	CIGIOCOGIT IGATAACAAT TATCICATAT TGTCTTTTTT ACCCACAAAT ACATCCACTC	600
	ATAGAGAGCA TTACCCCCAAT CCAGTICAAAT ATAACCGAGA ATTTGCATAT CAGTACGTGG	660
45	AATCOCAGCA GITGCTGTGA TTITTACTATT GATAACOGGC GCAGCATAAG GOCTGTGTTT	72
	(2) INFORMATION FOR SEQ ID NO:892:	
50	(i) SEQUENCE CHARACTERISTICS:	
	· · · · · · · · · · · · · · · · · · ·	
	(A) LENGIH: 726 base pairs	
	(B) TYPE: nucleic acid (C) STRANDFINESS: simple	
	CLI STRANDALINESS: SIDCHE	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1557UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:892:	
	GATCCGCGGA TITIGGGCACC ACAGGGTAGT GIGGCCGCAT CAAATCATGG CACACACGGG	60
20	ACGIGOGIAC TCAGOCCCCT TATTICATITI CAACAACACA TICATIAGGI CICATOCIAT	120
	AGCTICTIGGGC AAAGCCGGGC GCCTTGGGGC CTGTGTGGCC GCCAAGTATIC GCTTAGGAAA	180
25	ATGCTOGTGA ATGTATATTA TACOCTGACG CCACCATTGC AGTCACGTGT CATGTATGGA	240
	CITICCTICCE ATTRACTATIC CCARCARCCA TOTICATICCT ATCCACATCA ACTRICCACAG	300
30	CACCCATATG ATGCTTATTC ATACCCCCCC CCTATCCCCCA TCTTCTTCAT ATAAACCCAC	360
	TETTETACAC ATAGGICCAT TETCCTCTCA ATTCCAAAAG CTCATCGCGA GTGCAGATGA	420
35	AAGATCTOGC TICTTIGGIC COGCOCCAGG CGGCACCATC GTGGAATTIC AGTGCACAAG	480
	ATGITATTAG TCTTAGCCAT CAATTGATCA ACCAAACCGA GCCGGTTTAC CACAACGTGT	540
40	TACAAGAAAA GCCACCAACA ATTGACAATT ATATCATGCC TCTAATATAC CATGAGGAGG	600
40	AAACAGACCT GCTATGGAAC CAGTTGGTGT TTCTCCCCCAA TGTTTGGCCC GATCCGCAGA	560
45	TROGREAACC GROGAACAAC GCAACATOCA TGCTGGACGA CTGGATTATT 98000TTACGT	720
45	CAAAGT	726
	(2) INFORMATION FOR SEQ ID NO:893:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 708 base pairs	
	(B) TYPE: mucleic acid	
55	(C) STRANDEINESS: single	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1558RP	
10		
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:893:	
15		
	GATCTATTIT GOOGACTICC CITATCIACA TIATICIAIC AACIAGAGGC IGIICACCIT	60
	GGAGACCTGC TGCGGITTATC AGTACGACCT GGCATGAAAA CTATTCCTTC CTGTGGATTT	120
20	GOALACCIOC IGCOGITATO ADTACOACCI GOLATORAMA CIMITOCITO CIGIODATIT	120
20	TCAAGGGCCG TCGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	180
	ACCCCATCTC COGATAAACC AATTCCOOOG TCATAACCTG TTAAGAAGAA AAGATAACTC	240
25		
	CTCCCACCOC TCACCCCCAC GICTCCACAC TCAGTTACGI TCCCGTGAAG AATCCATATC	300
	CACGTTCCCG AATATTAACC GCATTCCCTT TCGATGGTGG CCTGGAAAAT CAGGCCTTTG	360
30		
	AAACGCACCT TOCOCCATCTC TTAGGATGGA CTAACCCACG TOCAACTGCT GITGACGTGG	420
		480
35	AACCITICOC CACITCAGIC TICAAAGITC TCAITIGAAT ATTIGCTACT ACCACCAAGA	400
33	TOTOCACTAG ACCOCGITICG ACCOCACCTYT ACACCOTAGG CTTCGTCACT GACCTCCACG	540
	ICIGIACIAS ASSOCIACIO ACCASCITI ALASCIASS CITOSIGALI GALCIGARA	330
	CCTCCCTACT CCTCACCCC TCATATTTCC CCTCACCCTC GAGTATACCT AACACCCTTG	600
40		
	AGOGCCATOC ATTITICAGGG CTAGITICATC GGCCGGTGAG TIGITIACACA CTCCTTAGGG	660
	GATTICCGACT TCCATGOCCA COGTCCGGCT GTCTAGATGA ACTAACAC	708
45		
	(2) INFORMATION FOR SEQ ID NO:894:	
	(i) SEQUENCE CHARACTERISTICS:	
5 0	(A) LENGTH: 671 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(b) torobost. Thich	

(ii) MOLECULE TYPE: UNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1558UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:894:	
15	CATCOSCIGG IGITITCTTA TGACCCACTC GOCACCITAC GAGAAATCAA AGICTTIGGG	60
	TTCT09099G AGTATOGICG CAAGOCTGAA ACTTAAAGGA ATTGACGGAA GGGCACCACC	120
20	ASCAGIGGAG CCTGCGGCTT ANTITIGACTC AACACGGGGG AAACTCACCA GGTCCAGACA	180
	CANTANCENT TEACACATTIC ACACCTETT CITICATTITIC TECCTOCICC TOCATOSCOC	240
25	TICTIAGITG GIOGAGIGAT TIGICIGCIT AATTOOGATA ACGAACGAGA CCTIAACCIA	300
	CTAAATAGIG CIGCTAGCAT TIGCIGGIIG CGCACIICTT AGAGGGACTA TCGGITICAA	360
30	GCCGATUGAA GITTGAGOCA ATAACAGGIC TGTGATGCCC TTAGACGITIC TGGGCCGCAC	420
	GCGCCCTACA CTGACCCAGC CAGCGAGTAT AACCTTGGCC GAGAGGTCTG GGTAATCTTG	480
35	TGANACTOCG TOGTOCTOGG GATAGAGCAT TGCAATTATT GCTCTTCAAC GAGGAATTOC	540
	TAGTAAGOGC AAGTCATCAG CTTGCGTTGA TTACGTCCCT GCCCTTTGTA CACACOGCCC	600
40	CTCCCTAGTA CCCATTGAAT GCCTTAATGA GCGCCTCAGG ATCTCCTTAG ACGACCCCCC	660
	AACTCCACCT C	67 1
45	(2) INFORMATION FOR SEQ ID NO:895:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 622 base pairs (B) TYPE: nucleic acid	
30	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1559RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:895:	
10	GATICCAGAAT CCAAGTTIGCG TIGTTCGTAGC AACCGCCCCC TGCGCAGGTT ACGAAGCAGG	60
15	CTAACCAAAA GCCCCTGGA TGCCCAGCAC ATCTCAGAAG TAGTACAACG CATAAAGGAG	120
	AAAAGCAAGC CAAGCGCTGA AAACAAGACC GTGCGTGAGC GGACTCCCTC ATCCGCTGCG	180
20	GITOCTGATC CTAAGAAGOG GGTAGTOGAT GTCCCAAACA ACCCGCCAAA CAAAGTATTG	240
	CTOGTACAGG ACCTGCCAAC AGACATTACC GAGCAAGAGC TGGTGGATAT ATTTGCAAAC	300
25	CATAAGTTOC TCCAGGTAAG ACTAGTCCAA GTCCCGCCAAC TGGCGTTTGT AGACTACGCC	360
	GATGTACAGA GOGCTACGOC GGTCAAGAAC AAACTGOGTA CAAATTATGT GATCAAAAAT	420
3 0	CAAACAACCA TCATAGGGTA TGCGAAGTAC ATAGGGCCGT GGGGATATGC GITCTTACCA	48
	GIGOGIOGGA ACCCGACAGA TCATTIAGGI AACTACATAA TGATAGTATT TACMAGACIC	54
35	CTTANGTOGC ACGIGOCTICG ATGICATTTC CCAAAGAGGA CIGITCTCAT AGCIGIGAGC	60
	AACGACTICTT TOCTOOGTICC TT	62
40	(2) INFORMATION FOR SEQ ID NO:896:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 643 base pairs	
45	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1559UP

55

	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:896:	
5	GATCCGATGA CCGTCATGIT CTTCTACAAG AACAAGCACA TGCGATGCGA CTTCGGCWCG	60
	GGGGAACAAC AACAAGATGA ACTTOGTOGT TGACAACAAG CAGGAGATGA TAGACATCAT	120
10	AGACACOGTIC TITCCOCCOCG CCACGACAAA CAACOCCCTG GTOGTGTCCC CGTATGACTA	180
	CAACTACAAG COGATACAAT AGAACATTIT TIGCAGCTAG TGTTGTCCCA CGATAGAAAG	240
15	TTTATACGCA ACCCGGCACA GGCGCCGGGT TGCTTGGCTC CACAGCTGGC GATGCAGCCT	300
	TOGGTAGGGC CUTGCTGGCC ATTATTCCTC TGACTCGACC TTACGCCTAT AGATGGTGTC	360
20	TGGGCTGTTC TGGCGGTGAT AGTGAAAATT TTTTGGCTTT ACGCTCCACC GGGTTCAGGG	420
	CTAGOCAGCA GGATAAGIAC WIAGGICITTI CIGCITCAGG CATTATATAA CCICAAGOGA	480
25	CCTTTTCAGA CCTTTTAGGC CAATATATCT CCAAAGTGTG CCCATCTGGA CTATTAAGCA	540
	GGAGGITICTA TICCAGOGIC ATCAAGAAAT CIGICAGAAT AAGAACCAIG GCCICAGAGG	600
30	ATGIOCAACT GOCCAGGAAG GCTGTTGAGT TTAACAGOGA GAA	643
	(2) INFORMATION FOR SEQ ID NO:897:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(D) TOPOLOGI: Timear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1560RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:897:	
55	GATOGOGG AGGITCIGTA AAAACCITICT ATICCAAAC COCACACCAT COTTO	

	GIOTOTICA AACTOOTICE CACTAATEGT GOOGLOGICO ACGACTITAT CATICOUGIC	120
5	AAACACTAAG TCAGGGATC	139
	(2) INFORMATION FOR SEQ ID NO:898:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 139 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1560UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:898:	
30	CATCCCTGAC TRACTOTTE ACCOGAATGA TAAAGTCGTG GACCACCGCA CCATTAGTGC	60
	GAAGGAGTIT GAAGAGGACG AGCGGGACCA TGGTGTGGGG TTTGTGCATG GAAGGTTTTT	120
35	ACAGAACCTC COCCCGATC	139
	(2) INFORMATION FOR SEQ ID NO:899:	
	(i) SPQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 688 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1561RP	

55

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:899:
5	GATCCAAATA ACCUTOCCGT CCATACAAAT GAACCCTTCA GTGA

5	GALCCAMATA ACCOLOCOGY	CCATACAAAT GAACGGT	CA GTGAAGCTAC TICGCTCGGT	60
	COCCIATGAT TACTCOCACC.	ADOCTICTICEA TICALOCCIO	DE COMEMICACIO CTOCTOCTMC	120
10	99CAGCCAAT ATATACATCT	TCTATAGGIC TAATICAT	GT CCOCTTTTTA AAAAAACCCT	180
	TOCCTCAATT TCTATCTACT	AGGCTATGTA ACGGCTCA	GT COGREGORIC GOCCARCOCT	240
15	TCCTGGATGG AAGCAAAGAG (CITITICGAAC TCTGCGTG	GA CCTCGCGCTC GCCGCGCCTG	300
	COCTOGRAGA ACTTOGRAGGA (CEAAACCCCC TGTTTCAC	GI CECCENTIEC CICCENCACE	360
20	ACGSCCCAGT TGGCGCCGTT (SCACACGCTC TTTTGTGC	CT CGTCCAAGTA GCACACAAAC	420
	OCTITICATCA TATOGIAGGI (TTCCAGATG GCGCAGAA	TG CGTCCTACCT CCACTAACCC	480
25	TICIOCIOCA AGAAGICITC 1	PITGATTAGE GTOGOGAC	AT CCAGIACGAT CTIGTCTITG	540
	TCAGAGAGGG CGCACTTIACC C	PACCAGCIGA ACAACTIG	OT COAATTOCTO GOOGTTOCAG	600
30	AGGATCICCT TGATACGGTC 1	CTCAGGACT GGGAACCG	OG GIAATIOCTA TCATAGTATT	660
	TOTTIMOGAC GITOGIGITIC C	TTOGAGT		688

- 35 (2) INFORMATION FOR SEQ ID NO:900:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 711 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDELNESS: single
 - (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: DNA (genomic)
 - (vi) ORIGINAL SOURCE:
- (A) CRGANISM: PAG1561UP
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:900:

40

	CARCOCAGAC TOTAGATOCAT GOTACIOCAGAC TOTAGACAC TOCATAGAC	60
5	TAAAAOCGAA GGAGACTOGG TTACTTGTAT GTTTTGCTGA OCTTCTGGTG GCAAAAGOGG	120
	TOGOCOCOG OGTOGGACAC TATTITIGGAG COGAATCAGC CTGAGTGTTC TTTTTGTTTT	180
o	CACCAAGGGC GGGTAACCTG GCGCCAGGGG CTGGCCCGGGG AGGTGATGGG CCATGAGGAC	240
	AGCAGGTATIC GCGGGAATAT GGAGTGTCCG GGGGCGCCCT TATGTAGACC CAGCACGGTC	300
5	CCCASCCATC GCGCGGAATT GCGCCTTTTG TAGAGTCCCG CTAGGCCCCC TGCCCCCGCC	360
	GTCAGCGCCT GTGACACAGA CAAATAAAAT TGGGCAAGGG GGAGACACAA GTCCCACAAG	420
20	COSCCACTOC ACGAAGCTAT GCACGCATTC AAGGAAGACT TACCCCATAC CGTGGGTTTT	480
	GCCCTCGACA ATGAGGAGAT CACATTCCCC AACTACGTGC CCACGCATGT GCAATCGTTG	540
25	CCCCACACT CCAACGGGAT CCGACAGCIA GTCATAGATA ACCAGAACCA GCGCGTCCTC	600
	COCACATATA ACCOCCTACT CEACCOCATE CAGGACOCCC TOGTGCOCCTC CCCCCCCCCC	660
30	GCCAGCTCCC ACGTCCGCTC CTCGCTAGCA ATCCACCGCA CGCACCCGTA C	711
	(2) INFORMATION FOR SEQ ID NO:901:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1562RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:901:	
	GATCATTICA GIGCAAAGGE AGAAGIAGGE CTITICACAG TACGICGOGT GIGTGGACAT	60

	CCTAGGTACT GITGACATTC ATGTGGGTCA GTCAGATTAC AAGTACACAA AGTCGATATG	120
5	ACAMOCCACG TGACCATATA TOCAAGACGC CCCCCAGCGC ACGCCTGCTC TGTGCATAGG	180
	ACTORCTACC TACCACTTAC AATOGGGTTT GCAACTTAAC TOCTCTAATC CTCACACGCG	240
10	GAGITATATA TGTGCTATAG GGCATGCTCC CGGGGCCCAA TTCAGGGCCA ACGGCCTGCC	300
	ACCATOCCAG AGCAGCCATA CCAAGCGCTG CAACAGGATG CGATATCTCG TTCTATATAT	360
15	ATACAGATAT ATATATATAC TOTAACAAAA TOOCTAGOGA TOTOOCTGIG AAAGGCCOGT	420
	ACTIVADATCA TATOGTOGIC TICTICAGOO COGATOGACA AAGOOOGOC ATOGTTOOOG	480
20	AASCITOGAA GCICOGGCC AGAAGADCTC AACTOGAGTG CCCCCCATAT AAAGCCCGTC	540
	ATGAAGAGCA TIGIAAATGC GCAAACITGG AAAAAGCCIG CIGGCAAAAG CAICACIGCC	600
25	ACCACCACIT CTACCACCCC COCACCCATC TAACTATACT ACAACCACCC CTATTCTTCA	660
	ACCASTOSTA CTGSTCGGAA TTCGAGGTAT ACCAGCAGGA CGGAGAGTOG AAGGCCGAAA	720
30	(2) INFORMATION FOR SEQ ID NO:902:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 592 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
40		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1562UP	
~		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:902:	
	GATCTGGCGT GCATATATAA CGIATCTGCG CTCACGCCAC CTGGTGCGCA CTTCTTTAGC	60
55	COOCTIACTAA CTCTGTAGCT GTTGGGGGTG GCTGCGGGGC GGCGGGGGA GCTTGGCAGA	120

	ATCCCCCOTT GCGTCALGGC CAGIGCCAG, CGAACAGGAC GCCCTTTTCT AGCAGCAGCG	180
5	CTTCCGCAGC GGITTCTTTT TTTTCCCAGC TAAGGIOGIG TATTTTCTCG CAGAGGGITA	240
	GAAAAGIACA CITTIACATCT GAACACACCA CAAAGIOGIT CIGAITIOGAG AGGCAGGAAA	300
10	CCAAACAATT GAAAGGTATG TTGAGTGGTA AGCAGACGGT ACACTGAGCT GGCCGTCTTT	360
	TAGCAGCTGG CGGCCACCCG CACTITICTCT TETCCCGCTC TGFTGCTTCT TGCGCGGCCC	420
15	CTTGGCCTGG ATCTCGAGAG CCGCGGAGCT ACCGCCCGTC CCGCGCCAGC CTGGGCTTCC	480
	CACCCCCCA GTGCTCACAG CCCCTCCCCC ACCCCACCCG GCTTCATGCG CCCCTCCCCG	540
20	CTCTGTTTAC AGGGATCGGT CACGTGCCGT GTGAGCCTAA GCCCGTGCCG AG	592
	(2) INFORMATION FOR SEQ ID NO:903:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 732 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1563RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:903:	
	GATOCTOGOT ACTITICACAA CATCAGGAAG GOGOTTOCTIG CAGGOTTITIT CATGCAGGIA	60
45	GOGAAGAAAC OCTOGGGAGG GAAAGOCTAC ATTACTATCA AAGACAACCA AGACGTOCTC	120
50	ATCCACCCTA GCACGGICAT TGGCCACGAT GCAGAGTGGG TAATCTACAA TGAATTCGTG	180
50	CIGACIACIC AAAACIACAT ACGGACGATC ACCTCCGTCC GICCIGAGTG GTTGATTGAA	240
55	CICOCACCIG CGIACIATGA CCITGATAAC TITICAAAAAG GIGATATCAA GCICAGICIG	300

	GAACOCATTA AACAAAAGAT GGATOOCATC GAAGAGCTAA GTAAAGAGCA ATCCAAGAAG	360
5	CATACACAGA GCCGCGTA NTTCGTGAGC TTGTTGTAGC TAAATATCTC TCTGATATAG	420
	CATGIACACA ATAATAGGAC TTTTGAGCIG TCCTTCGTTA CTTCGGATTA GCAAATTATC	480
10	GCAGAAGTTA GCAGGCACCG CCGCCCTTGT TGGTGCGCTT GCACGAAAGC AGCTGGTGAT	540
	GTTCGGCGTC GCTAAAAACC CTCATTTGTG CCTATCATAT GCCCAGCGCT ACAGAGTCTT	600
15	COCATCATCA TOTTICAGAA GGACGAGATA CTCCCACTIG ATGAGOCCAG GTCCCAAAAG	660
	ATAMAGGAGT TOCTGAGCCT CTCCCTCGGG CTGATCACCG AATCCATCGA AAAGAAAGAA	720
20	TATGACICCA TA	732
	(2) INFORMATION FOR SEQ ID NO:904:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1563UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:904:	
45	GATTORETTIET CTTCCGACCC TOGTACACCG CTGCCGATGCG CETCTCCCCC TGCCCGTGCA	60
	TATOGGAGAT ATGGCGCCGT GCCCGTACGG CAAAGAATCA GCAAGACACT AGCGTCTGGC	120
50	ATTCTTTTC AATGCATTAT TTAGCTTTTT TTTTTTTTTT	180
	ATAAAGIYAGA GITOGICATO AGTAGOOCIC GIAAGGITIAG GOOCOGOCIT CACGOCATAG	240
55	TAGCATCTCC GTCAGACTCC TGGATTGGCG CTTGCTCTAT GCCGGCGGAT TCCGCCAACTG	300

	COTAGOGICT TICGITAGOG GACTOGTTCC CACOGGCGGC ATGGGCAGGC CACGAGGAG	360
5	CTCCCGTTAGC AGCCTGTGAC TTGTCTGGCA GOGAGGGGCC TGGTGGGTGC TGGAAGAAGC	420
	AGTICOCCGTT CCCACATTCC CCCCCCAATT TOCAGGGCTC CTTCATCCCC TCCCCCAAAA	480
10	ASCAAICTAT GCGCGTGCAC GCAGCGCCCT CGCGGCACAT AATGTGTGAA CGCGCATGGC	540
	GETACTIACA COGITTIGITIC GIBCACTIGA COCCGAACIT ACACTOCTOG AGGGAACOCT	600
15	CCCCTGGTGC AAACGCACCG GCTTGGAAGG ACGTGGCGCA GCAGCAATAG GCTGAACATC	660
	TOGINTOTTE GACAAGGAAG ATGOGOCTTE TOGCAGTOOT CITETCACAG GITTAGET	717
20	(2) INFORMATION FOR SEQ ID NO:905:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDHINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1565RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:905:	
	CATCACATOT TITOCOCAGA CACOCACCTG COCTTGAGAG ACCGATGCCC CCTTATACCA	60
45	CTGAGCCCTA TTAGTTGCTG GATTTGTGTT TCCAGCAGCT GCGCATGGGG CCGGATTCCG	120
	TCAAGTGTGA TTCCGCAGAT GTTGGTTTTG GCTCGATAAG TGCATAAGGA AGCTGCTCTG	180
5 0	TTAGTACATG TCACATAGCA COCTICCOCA TTOCCCATG CCATCCAGTG CCCCCTTGT	240
	GOCGCGACGG GTATTCCAGT AGCCGTCTGC GAACOGTATT CAATCATCTT TGGCCCAGCG	300
55	GTATATAAAG COOCTGATGA GCCTGGATGC AATGGGGTGT AGCTGCGGAG ACTGCACCGA	360

	ALMOTOR & GRADITION PROCESSION AND AND AND AND AND AND AND AND AND AN	420
5	TITITICIASC CCAGICCAAG GOCTACTITIC AGCAGGAGGG TGTGGACATT GCGCTGCTCG	480
	ASCCCACGAA CCCGTCCCGAC GTGACGGAGT TGATCCGGTCC GCGCAAGGTT GACATGGGCC	540
10	TARACCOCAT GATCCATAGG CIGOCCGCTA ACCCACGIGG TITICCOCGGIC ACTITCTGTTG	600
	CATCOCTOCT GCATGACCCG TTCACCGCCG TTCTGTACCT GCGTGGCAAC GCAGTCACAG	660
15	ATACTITICAG CICTCTICAG GOGAAGOG	688
	(2) INFORMATION FOR SEQ ID NO:906:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 558 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1565UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:906:	
40	CATCCCTITC ATACAGGICA ATATTITATG CAGAGACAGG GOCTGGACGT TGTAAAGGTC	60
	TTTCATCCAG ATATOCTAAG AGGCGAAATT TCATGCACGA GTATGATCAC AAAAAATGAC	120
45	ACAGCCAAAC AAATTGCCAT TATTTTTAGA GCATCTACAG TGATACAGGA TTGGATTATC	180
	CATGITCIAT CCACCCCIAT TOCATICATT CICGCTCCTA CCCCCTATCA GCCCGTCAGT	240
50	GCAGCTGCAA AGTGCCCAGG GAACTIGTCTC ACGCACACTG GCGTCTACGA TCAATTTAAA	300
	AAAGCATTTA AGGATATTTA TOCTGTTTTT AAGCCGCTAA AAGACACACA TCCGGATTAT	360
55	GAGGICATAG TTACTOGICT TTCCTTAAGT GGCGGCTATG CTCACTTTAT GGGTATTCAA	420

	TIGCAACTIC TGGGCTACAA GCCTCATGIT TGCGCCTTTG GATCATTGGG TATAGGCMAT	480
5	AMEGACTITA ACCATTOCCT CCATGATATA TITCCGTCCG AACACCTTTC CACAACAATC	540
	CCAAATAAIG AGATOCCC	558
10	(2) INFORMATION FOR SEQ ID NO:907:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 645 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1566RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:907:	
	CATCOCCAAA CACAACOCOC GOOGOCOCOT ACOOCOOCOG GOOGTOCTOC ACCACGTOCO	60
35	CCACGCCCTC GCGGCCACT ACCCCCTACC ACTIACATCAA CCCCTIACCTG CAGGACCACT	120
	COGTOTTCAA CAACOCOOC GOCOCTATOG GOCACATOCT CATTCTOCAC GCGTCTGTCA	180
40	COCAGNACOT GATTETETIC COCACOCCOG TOCOCACOGA COCCOCACAGG GCCGTGCACT	240
	THOCOGATGA CTACTICACG AUCCHOCACG GOGAGCAGAG CGCGGCACTG CCACACGCCC	300
45	TOCACCOCCA OCTICTACACC COCCUTATICA COCCATICACCT COCCATIGOCC CACCOCCAACC	360
	ACTACOCCAT GCCGTCGGCC TCTTTTGCGC TGGAGCTGGC ACAGGGGTGG ATCCCGTGCA	420
50	TOCTOCCGTT COGTTTTCTC GACACGTTCA ACAGCACACT CCACGTGTAC ACTCTGGCGC	480
	GCACCGIGCA OCTGACAGCG COCGACATGT TCAAGAACTT GGTGTACAAT TTCAAGITTT	540
55	AGCCTAGATA CATAACCACC ACCAATGTCT GCGCAGGCCT CGCCCGCGAC AGAGCTGCCA	600

	GAACCCGACG CTCGGGCCAGG TGTACGCCAC GCTGACGGGC CACTC	645
5	(2) INFORMATION FOR SEQ ID NO:908:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 701 base pairs	
10	(B) TYFE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1566UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:908:	
25	GATCCTCAAG TCTACGAACG CCTCCAAGGT GTTTACCACG GCCGTTTTGG CTCATGTCAT	60
30	CACACCICAG OCTAAGOGIG ATTITICACOC GAAGICIOCT GICCCAGGIC ACGIGCAACA	120
	GOSCOSCOTA CCATOSCICAA TOCACAGAAC CAGAGGAACT CGTICTOSCIG TOCGTIGOGAT	180
35	COOCTICATO GAGOCTAAGO AGGACGICAT TOGOGAAGOO AGGGGAAAAT GAGGAGGOOT	240
	THEACHGOOC CGACAAGOOC GHCTCTCACA COGCCGCCGT CCHCGGCATC ACCGCCTCCC	300
40	AACTGAAGTT CACCTCCATC AGGCAACTCT AGGACCTGGA AACAGAGTTC TCCAAGGGTA	360
	TOCCAAAGGT TATCCACTGG GAGGCTACCC GCGCGATTGC GGACCATTTA GAAGGCCGCA	420
45	ACAGGGTAAC AGTITAGIGT CICTGTTTCG CCCCCTGCCC CACTATATGT ACCACTACAT	480
	ACCACGATTA TOGATAAACT TAACATOOCA GAGTACACTC TOATOCACCT GOCATGIATA	540
50	TAATGIGATT TTACTGACCA AAACTGTTTT AAACGCCGTT GCAGGGTCCG TCGCAGCTCG	600
	TATAAATATC TIGACGCCAC CICGATCICC ATTOGIGAGG AAGIACCCGT CGAGATACAA	660
55	TAGTGCCAGC TIGCTAAGGG GTAAGCTGAC CACTCTACAC A	701

(2) INFORMATION FOR SEQ ID NO:909:

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 697 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1567RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:909;	
25	GATCAAATGC CCTTCCCTTT CAACAATTIC ACGIACTTTT TCACICTCTT TTCAAAGITC	60
25	TTTTCATCIT TCCATCACTG TACTTGTTCG CTATCGGTCT CTCGCCAATA TTTAGCTTTA	120
30	GATOGAATTT ACCACCCACT TAGAGCTGCA TICCCAAACA ACTOGACTCG TOGAAAGAAC	180
50	CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTICTCAC CCTCTATGAC GICCTGTTCC	240
35	AAGGAACATA GACAGGGACT AGCAACCAAG GTACTITICTT CAAATTACAA CTOGGACGCC	300
	GAAGGCCCA GATTICAAAT TIGAGCTTTT GCCCCTTCAC TOGCCGTTAC TAAGGCAATC	360
40	CCGGITGGIT TCTTTTCCTC CGCTTATTGA TATGCTTAAG TTCAGCGGGT AATCCTACCT	420
	GATTICAGGT CAAACTTIGG GAATACTATT COCCTGGAAG GCCTIGITIG TCGTACGITC	480
45	TTCAAGCGCC AGCTCCACTC CACGATCTGG TCGAAACCTA ATACCCAGTG TAGAAACTAG	540
	CTCAGACOGC AGTCCGCCCA AGTTCCGCCCC ATGGCCAGCA TTTTCAAGTT AACCTTGTCT	600
50	TACGACCCAG TATCACTCAT TACCAAACCC GACGGITTIGA GAAACGAAAT GACGCTCAAA	660
	CAGGCATGCC CCCTGGAAAT ACCAGAGGAC GCAATGT	697
	(2) INFORMATION FOR SEQ ID NO:910:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1567UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:910:	
	CATCGICAGA TACCTTAGIC TCTATACAGC GCAAGACATG GGTGATOOCG GGTTTGITCT	60
25	ATGEAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC ACCTGCCTAA CCTGAACAGT	120
	CICATCCIOS OCATCIACOS ATCCCATOGO TGACCACCOS ACCATITOGI OCATTACTAG	180
30	CCAATGGCAA TCCAAACCAA AGAAACCGAC TIGGGGGAAT GCCTCAITGA ATAGCGGTG	240
	THTCGACACT GIGATICICI GAGIGIAACC TOCTCHTIGG THOCOGATAT TAAACCTGTT	300
<i>35</i>	CIGIGAAACA TOGGAGOGGI GITTAGIGGA AAGCAACTAG AGCAACTCAA AGAGIGCTAT	360
	GOCATGGGGG CACCIGITGC GAAAGIGIAA AAACCCGAGC TCCGGTTCGC TTGACACAGA	420
40	AGITACITIC IGIATUTUIA TUAGTUTATU ACOGRAGORO OGTOGTOTO TITTOCOCATT	480
	TICOGGITGI TOTTTAAGAT AGITATOTIG TIGATOCIGO CAGTAATOAT ATOCITGIOT	540
45	CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTTAT ACAGTGAAAC TGCGAATGGC	600
	TCATTAAATC AGITATCGIT TATITIGATAG TICCITTACT ACATGGATAT CIGIGGIAAT	660
50	TCTAGAGCTA ATACATOCTT AAAATCTCGA CCTTTTGGAA GAGATGTATT AT	712
	(2) INFORMATION FOR SEQ ID NO:911:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 696 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1568RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:911:	
20	GATCACGAAA COGTCOCTAT TAGGITCCCA TGCAAAGCGC ATGCAGCGGT CCTTAATCTC	60
	CACCITCICA AATGGAAACT CICTGGCAGT CAAAGAGCAA ATCICCATGT TGGTGAAGAT	120
25	GGICTICCIA CACTICGIGI CACCGICCAC CIGIACACAG ACCAACICIG CCICGTICIG	180
	CCAATIGGAAG GAGACATCAG TAACCTGCAC CAAGITGATG GTACGCAGAA CACGGGGGTT	240
30	COSTAGCICA ATCAGCACAG CITTACAGCA CIGGITGITC GACTICIOGAG TOCAGTATAC	300
	CATGACAGIA GATGGIGGGI CGTIGGGICT GITTIGACGCC AACTTGATGC CCTTAGCAGC	360
35	AAAGGAGAAG TOOTGAACAT OOTGGATCTT CATCACCTTA OOGGCCAACA GOTGGAAGTT	420
	CTTCTCGGTC TCGTACACAG CAATTGCGCC AGGGCCAAGA CGAGCCCAGA ACTTGTCGTC	480
40	AAAGGACCAC TIGACCATAG GCCATTGCAG CTGCTGCTGA GGCGGCAGCG CAAAGGTCTT	540
	CACGCAGACA CCTGTTGCCA CATCCCATAT ACATAGCTGG TGGCCCGGG ACTCGGGCCC	600
45	GAATGEACAA GOCTOGTTAG GTTCATOCGA GACTTCTAGA GGTTCOCGAGG AAAAGGTAAC	660
	CAGGTACTTC TCGGTCGAGG ACATGGAGAT CGCCTT	696
50	(2) INFORMATION FOR SEQ ID NO: 912:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 697 base pairs	
5 5	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1568UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:912:	
	GATCATCTAC GIGOCCCATG AGGATAATAA GGAGAAAGAA TICGAAATIG AGCTGAGCIG	60
20	GTGCTCCGCT TCGCACACGG ATGCCTTGCA CAAGGGAGGT ACCAAAAGAG CTATTTGATG	120
	CAGCGATTCA GTTTCCCAAG AACCACACOG GTCAGCACAG TGATGATCAT TCAAGCCATG	180
25	ACAACGCATC TOGAGGTGAA GAGTCCTCAA CAAAGAAGGA TGCTGACGGT GATGTCCAGC	240
	TITCATGATA ACAGCCCGGC ATTATGTGGA GGTTCATTTC ATGACAATTG ACGGATGTTA	300
30	CTAAGTGTAT ATTAAGTTAA TOCACCTATA TAAATTAATA ACATGCAAAG CAATTTAGAA	360
	TITGICCGAA AGCAGGITAA AGCATGICTA CICTOCITAA TCTTTCCCCA AGCTGIACAT	420
	THTCHTCHIC AAGUGAACGA ATHCHATCCA CGGCTGCGTC TGATTCHAAT TTCCTACGTT	480
	COCGITCIGI GIACCATTIC COCGICACCI CITCIATCAT TAATTITICAA TOCTGATCAA	540
40	ATGIATCICA TICATOCCAG COCTGOCACA CCTGOCATAG ACGITTCATT CITICTICTCT	600
	TITCCTTIAA CAGCAGCTIT ACATGITCCT CCACTATTGA TGATGIGGCA TITTGGCATG	660
45	AACATATAAA TAGAATOOCA TTTCAGCIGG TTTCTTC	697
	(2) INFORMATION FOR SEQ ID NO:913:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 672 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1569RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:913:	
15	GATCCGATAT ACCCTGAGTG CTATATTACA AACCATCAAT TIGATGITAT CTTCGACGTA	60
	TIGITOGITA ACCAÇACGAA ACAAACTITIC AAAAACTITOC ATGCCCAGIT TGCCAACCCTG	120
20	GOOGACCIGA AGATIATATG CAACCCTCCA AGCACCAATC TAGITCCTCA TGGITTCCAC	180
	AGATTTAGOG TTACAGTGAA GGTTTCAAGT GCOGATACTG GTATAATCTT TGGGAATATA	240
25	GITTATCACG GIGGACACGG CGAACATOCA COCTATGICA TCTTAAATCA TGTCCATGIT	300
	GCTACAATGG ACTACATTAA GCCTGCAGTT TGTGATGAAG CTTCTTTCCG CAAGATGTGG	360
30	AATOCATTIG AATOGGAGAA CAAAATOGIT GICAAATCIA AGCIACOGAC TCIGCATGAC	420
	TACTIGAATA ACCIGATIGA GGICACCCAT ATGAATGICC TGACTCCTGA AGAATCATIT	480
35	GCCGACCCCG AATGICGTTT CTTAAGCTGC AACTINTACT CGAAGTCCAC CTTCGGCGAG	540
	CATOCTOTOG CITATTIGIC TATOCAGAGA GACOCTACTA GIGGITOCAT CATOGGAGAA	600
10	GITTOSCATOC GCTOGAAGAC GCAGGGCCTT GCTTTGACCC ACGGAGACAG TATTIGGGCMC	660
	ATGCAAAGGT CC	672
5	(2) INFORMATION FOR SEQ ID NO:914:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 698 base pairs	
0	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	· · · · · · · · · · · · · · · · · · ·	

(vi)	ORIGINAL	SOURCE
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(A) ORGANISM: PAG1569UP

10	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:914:	
	GATCIOCAAT CCICTICAAC AATTICCTCC AACCIATICT CCIGATGACC TIGCCATCIT	60
15	GAGTGAGCTT TTTGATTCCA ACAGCAAATC TGAATAGGCC TCTATCTCCT TTAAAAAGCAG	120
	CGTCGTOCAT GGGGCTTTGG GTTTACATTG GAAAAAACCC CAAAGAACAA GGTAATGCAT	180
20	GCCAAAAGIA GCCTTTAATC CACITCACAT TIAGATATIG TIAGGCAGIG TAICTATACA	240
	AAAAATAACG ACAAATAATA TCTTTTAGAG CTGGTTCTTT ACACTAAAAT AGGGCTCGGT	300
25	ATOCAATACC TCAGATOCTA TCTTGATATC CGTGTGGATA TCCTCGATTA AAGCCTCTTT	360
	CUICUICIA TITAATICOG COCCATUIA COCAACCAAC CICAACTIAA TITITOCCOCC	420
30	ATAGAAGTCT TCTTCAAAGT CGTTTAAAAT GTGCAACTCA ACCGTCTTCT TACTGTTGTT	480
	ATAGAACGGG TTCCATCCTA CCCATAACAC GATTGGAAAG ACTCCACGCT CTGTTTCCCA	540
35	CACCTIGGAG CCAAAGITGI ATATCACCTC GCTCCCATCA TITICTGTGAT GOGACCTGCG	600
	CTTCTTGGTC CATATTAGCC TTAACCCGGC CCAGCCAAAA TATACTCCTG TGGCCATTTC	660
40	GITAACITCC CTAGOCAATT GITCINTTOG GAACATTC	698
	(2) INFORMATION FOR SEQ ID NO:915:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SCURCE:	

(A) ORGANISM: PAG1570RP

5	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:915:
10	GATCCACAAC ACACACACCT TOOGGACTCT TTTTCTCAAA GACAGTTCAC CAGTCCAACA
	CTTGCAAAAC CATCTGCTAA CGTTTCAACG ATTGCGCAGC AGCAAACCCA GCCAACCGCT
15	CTCTCTCAAT CTCATCCTCA GCAACAACAA GGTTCACAAG CTCAGCAGCA GCTACTTCAA
	CAACAACAAG GITCACAAGC TCAGCAGCAG CTACTTCAAC AACAACAACA GCAACCACCA
20	CCACCACCAC CACAACCACA GCAACAAACA CAACAACCAC AACAACCACA ACAGCAGCAG
	CAGCCCCAAC CTCAACCGCA ACTACAACAA CAACAACAGC TTGGTTTACA GCCTCATCAG
25	CCACAACTOG COCAOOCOCA GOCOCAACAA CCACAACCOC AGCAGCAGAC OCAGCAGCAGCAG
	ACGCAGCAGC AGCAGCAGCA GCAGCAGCAG CAGCAGCAGC AGCAGCACACA GCAGCAGACA
30	CAACACCAAC CACAACCACA ATTGAAACCA CAATCACAGC AACCACAACC GGTTCCACAG
	CAACTCCACT CTCAACAACC ACAGCAACTC CAGTCTCAAC AACAACCACA GCCTCAGCAA
35	CITICACAGO CIGOCCAACA ACAATOGCAA CAACAACAGO AGCAGCAGOA GCAGTOTCAG
	CAGCAGAAGC TTCGCCAAGT GCAGCTGC
40	(2) INFORMATION FOR SEQ ID NO:916:
	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGTH: 714 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
- 55 (A) ORGANISM: PAG1570UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:916:		
5	GATCTTCGGG CCCGCGGGCC CGCTGGGCTA CGTGCTGACG CTGTATGGGA ACGCGCAGTT	60
	CTTCACAACC ATGATCGTGA ACTCGCACCT GGCGACGCCG CTGTTGGACT ACACCATTGC	120
10	GICOCTGATG GGTATCCATA TTGAGTACAA GCCCCATAAC CCTGAATTGG TGGAGCCCGA	180
	GOOGITICAGE GEATALGATG TOCTGALOGGT OCTGODOCTG GTCATGAGOG TTGCOGTGAT	240
15	GETGETTCTG GTGACCATCC CGATTCTGGG ACCTGTTCTA CTGATGTTTG TGATGAATGT	300
20	AAAGTTTICA TACGACTICI ACGACCOGIT CTTAATTCTA COGOGACTAA ACCAGGIGCA	360
20	GCGCCGTGAC GTGTTCTTACC AGCATATCTT ACAGTTTGCA TACTTCGGGG GGTCGTACAC	420
25	GETTPTAAAT TTCGTGCCTC TATTCTCAGT CTGGGGCTTT GTGTGCTATC CGTTGGCAAT	480
-	CAAAATGTGG GCGACTTCCA ACATCATCCA CTTTACAGCG GAAGAAGTGG AGTCCATCAC	540
30	TGAATGAAAT CATICATITA ACATGIOCAT CTATACATAA AGATAGATAT AGCCAGAATC	600
	ANTACCCIGC CCATTAGIAA AGIACCATGC TGTCGACACA GCCGAATCCC GCCCAACACC	660
35	OCCUTOGITG CACCAAGGCA ACTICCAACG CACCAGCCAT COCAGOGTAG TOGT	714
	(2) INFORMATION FOR SEQ ID NO:917:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 658 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1571RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:917:	
5	COCAGOCOGT AGGCAACACC GTTOCATATC TOCACCTGOC AAAGGTCCTG ACCCGGCAGC	60
	AGAAGCTCGC GCGAACGCGT AGTCCACGCA TACAAGTCGC CGCGGCGGTC GATTGCCAAG	120
10	TIGCAACCCT CCTCTGCCAG CGCCACATCC CGCAGCCGCT CGCCCTCAAA CCCCGGCACC	180
	COCAACOGEA ACCOCCTOCA COCAGCOTOC TOOCOCAGOC GOGOGOCOCA GTAGTIAGAGC	240
15	CCGGGGCICIC CIGGGCIGGGG CGGCGCCACC GGGAICTCGG GGAICCCGGG CAGCTCCTTC	300
	TIGOGOTICA TOTOCTICAS COSCICAASO SIGTISTOST COACCOSCOS GIOCOCOSCI	360
20	AGAATOCAGO OCTIGATOTG COGOCATTGA AGATACACOG TGOCTGCTAC TOCGATOCOG	420
	ACCACCACCG CCAGGCCCTG CAACACCGCC ATCAGCTTCT GCATCTTCTC CACCTTGTCC	480
25	GCATACTCCT GCTCCAGTTG GCGCGGCGAT TTGTCACTCC ACTGGTAGTC CAGCTTGCTG	540
	COCTIGUECT TETATETOCC ATOSTICAGE TOCTCITOCC ATCATCTOGG OCTCATCAAA	600
30	ACCCTGCCCC TTGCGCAACG CCCTTGCTTC CATAGCGAGC GCCTGGCCAC TCGCAGCC	658
	(2) INFORMATION FOR SEQ ID NO:918:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 657 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) OPICIDAL COMPOR.	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1571UP	
	(A) Ordanizari: Pareto/IOP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:918:	
55	CATCACGIGA TOOGATGAAA ACTICTGACAA ATOCACCOGG AATATATAAG GCATGGAGCT	60

	GCGGACTCGG CCAGACAGTG CGAGCAGGA AACAACAACA TCATCCAAAA TCXXXXAGA	120
5	ACCAGCTAGA TOCTACOGTT ACCAGAAGAA CAAGOCTTAC OCAAAGTCTA GGTACAACAG	180
	AGCTGTGCCA GACTCCAAGA TCACAATCTA CGACTTGGGT AAGAAGAAGA CCACGGTTGA	240
10	TGAGTTCCCT CTATGTGTGC ACCTAGTGTC CAACCAGTTG GAGCAGTTGT CCTCCGAGGC	300
	TITTOGRANGOC GOCCOGTATCI GTGCCAACAA GTACATCACC AAGATGACCG GTAGAGACTC	360
15	GITICCACTIC AGAGICAGAG TOCACCCATT CCACGICTIC AGAATCAACA AGATGITIGIC	420
	GIGIGCAGGT GCAGACAGAC TGCAGCAGGG TATGAGAGGT GCCTGGGGTA AGCCTCAGGG	480
20	TTTGGCTGCC CGTGTCGACA TCGGCCAGAT CATCTTCTCC GTCAGAACCA AGGACAACAA	540
	CAACGACATC GITGITGAGG CTTTGAGAAG ACCAGATACA AGTTCCCAGG TCAGCAGAAG	600
25	ATCATCATOT CCAAGAAGTG COGTTTCACC AACTTOCACC GTGCCCAGTA CGTCAGA	657
	(2) INFORMATION FOR SEQ ID NO:919:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 625 base pairs	
	(B) TYPE: mucleic acid	
35	(C) STRANDELNESS: single	
.5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1572RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:919:	
50	GATCTATTAT TAGAGGTAAT ACATTTAAAC TATTATCTAA ATTCTTCTTC TTCTTATTTA	60
	TICTIAACTI TATCTIATIA GGIAAATIAG GICAATGICA TGITGAAGIA CCATTIATIT	120
55	TAATAGGICA AAITIGIACA TITATTTATT TIGGTTATTT CITAATCTTA GIACCIATTA	180

	TITCTATAAT TGAAAATATI TIATTTIATT TACTAAAIAA AAAATAATAA TIAAAIAAAT	240
5	AATAATAATA TICATTAAAT ACTITAATAT TAATATITAT ATAITATACT ICITTATCAT	300
	TTAGGAGGGT ACCICATATT GCTGACTAAC AATAGGGGGG TGAACCCTAC GCACCTAAAT	360
10	GATAAGAGIT TATCATTAAA TTATATACTA TATATTATAA GTAAATTATC AAACCATATA	420
	TAAGGTATAT ATATTAAGAA AGTITIGACTIG AGTIGGTITTAA AGTIGTAATAT TIGAGCTATT	480
15	ATAAATCITT ATGATTICCT AGGITCGAAT CCTATAACTI TCGTATTAAA TAATTATITA	540
	AAATAATTAA AAATAGIYAA TAATAATGAG AACATGATGI TGGITCAGAT TAAGOGCTAA	500
20	CTAAGGGACA TTACACATGC CAATC	625
	(2) INFORMATION FOR SEQ ID NO:920:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 677 base pairs	
	(B) TYPE: rucleic acid	
	(C) STRANDFINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
3 5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1572UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:920:	
45	GATCCGTGTA TTTTTTATTT ACATTATITA ATTAAAAATA ATGATTTAAA TAAATATTTT	60
	TIATAAAAA TAATTAGIGC ATTGITACAT GITCATTAAA GAATGATTAT TATCAAAACC	120
50	ATCAACTAAT TGITATATAT TTATTAAATA TTAATTTCRC TTAATTAAGA ATTAGGAACT	180
	TEATCEATEA GICIGOGUIG TETCCCETTE GATTATTAAC CETATCCCTA ATAATCEGAA	240
55	ATATTTAATT TTAGATTAAT AATATATTCT CAGATTTAAT ATTTTTAATA AAATAAATAA	300

	TTATTCCCTA AATAATATTA ATAACTATAC CATATATAT	360
5	TAACATATGT TICGTAGAAA ACCAGCTATT TOCAAATCAG ATTIGACTTT CICTACTTAC	420
	CATTATTCAT CAGATAATAT TOCTACATTA ACCIGITCAA TOGTITITAT ATTITATTAT	480
10	ATTITAAATA TAATAAATAT ATATTITAAT CATTIGATAA TAGIAAGATC ATCIGCTPTC	540
	COSTTAATTA ATATTAACTA AATITAATTT ATTTTAATTA ATTTTAACAT TGITAAATAT	600
15	TTATATTATT TTIAATATCA TTTTTTATTT TAATATTATG CTAATATTAA TIACTTCCTG	660
	ACCCATTATA CAAAAGG	677
20	(2) INFORMATION FOR SEQ ID NO:921:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 623 base pairs(B) TYPE: nucleic acid(C) STRANDEINESS: single	
3 <i>0</i>	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1573RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:921:	
	GATCCGIAIG GAAATTATTT TITTATTIGA ATTATCTTIC TCCAGAACAT CCAAGAACAG	60
45	TGTCAGAGIG GT000CAGAT ATTOOCTTAAA CTCTCCTTCC AAAGATTTAG AAATTAGATTC	120
	GATAACAGAA ATGATTGTAA TTTGCAGTTT AATAAATGGG AAGAACICTT TAATGACTTC	180
50	AAATATTICG TCAACATATG GOOTGATATG TIGOTTCACA ATTGATACCA TAACACCTAA	240
	TIGITGAAAA TAAAACTCAA GTATTGATOG AOGACAGCTA COCATCACAT TAATCATTCC	300
55	TOGAATAATT TOCTTTAGGA AGGAGACOCA OCCGAGTCCC AATGTTTOGA AGATGTGCAT	360

	CACIOCCIGI AIGACACCAG IGIGAIGAGA AGAIAAAGAA GGAICCIICA AAAITIICAT	420
5	TAGAGTATIG ATCACGACOG TIOGATAATA TICTICATIG GAGGGIGACA TACCTIGCAT	480
	TAACAAAGCA ACATCTATGG ATGGGGCATT TTGTTCGACG GATATAGGCC TGCTGGATGT	540
10	TOTTCAACT TOTCTATGIT TATAAGGGTC CAGAGCTCCC AGAATCCCTA TTAGTCTAAC	600
	TGTPTCCCTC CTTATCCTTT G3G	623
15	(2) INFORMATION FOR SEQ ID NO:922:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 715 base pairs (B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(b) foroizer. Tilker	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1573UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:922:	
35		
	GATCSGATAG GACAGGGAGT AGGAGGGCCC CTGTGCCGCT GCCAGGGCCCT CGTTGCCAAT	60
40	GTAAAAGTCG AGGTCCTCGG TCCCCCCCTT CCCAGCCAGG TTGTTCGACA TCAAAGAAGA	120
	TCACCIAAAG CXXXICAACG ACCTCCCCCA CCICCICTTC CCAAAGAATG CACACCCCCC	180
45	AGOCCOCATA COCCIOCOCC TOTOGOCCAT ACCOCTICATA CTGCTACTCT TGCCCGTCTT	240
	OGAAGOCTOC OCAGTOCCAA TIGOCCTTOG GAACACCCAT GAGGOCGAGT CGTTACCTOC	300
50	AAATCCCAAT TICGTCAATC CTGTACCATT GTCCATGACA ACAGCAGGAT TATTGAGGIA	360
	TGACATOCTG TATTCCTGGT CTCAAATGCT TCTGGTAGAC TTGTGTGAGC CTTTGGCTTC	420
55	OCATOCCTTG TCACTTWCTG CCTTAACACT OCTGOCACTG GAAAAGGGGT CTAATGCGCC	480

	THICGITTIA GGIGATCACC ATCACCAACC ACGGIACACC TGACGAAAGG CAACGCCGIG	540
5	CONTROL COACCACACA CONTROL ATTOCOCCA COCAATTOCT COCCUTUTOC	500
	GITCCTCCAG COCTCCTOCT CCATCTOCCC TCTTCACTCG TTTATCAACC TTCAAACACG	660
10	OCATATAGOG ACACOGACTT TCTGCAGGTC TGTAGAGTAG CCCACATCCG GCGAA	715
	(2) INFORMATION FOR SEQ ID NO: 923:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 602 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(and a contrary contrary	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1574RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:923:	
	Chillipperson NC Company many among a series and a series	
35	CATCCCCAAG CTOGTCTGTT TOGAATTCGG GATATTTTTIA GGAAGTACGT TTGTTCCAAC	60
	GACGITOCIT CCATOCATCT TOCOGOGTIG TIGACOCAAC AUTITICAGIC TCACATICOC	120
	The second in th	120
	TGAACACCTT TGCTATCTAC TAGGAGPTAC TGAACCTTTT AATGTCTGTT AATAAATCTT	180
40		100
	TTGAGTTAGA TAATTCCCTG COCTACAGIC TOCATGGGIT TTCATTGCCC AACCCATCTG	240
	TAACTCTAAT TGAAAGGGAG AAGATCCTAT ACAGGAAATT AACAAAGGAG TCTGTGGCAC	300
45		
	TAGTITCCCC TCCCCCCTCC CCACATGACC CTCCCCACAG CCCCTATGTT GCCCACCCCA	360
50	TGTTAACCOC GOCTGTCOCA GGAGACATTT TTGCGTCOCC GTCGACGOCT CAGATTTTGA	420
50		
	CTOCAATAAG GATTOCTACA AAGCAAGCAG CTOGAGCATI OCTGATOGTG AAGAACTATA	480
55	CTGCCGACGT TCTTCACTTT GCCCTGCCAA CTGAGCGTGC TCGGTCTATG GGCATTGATT	540

	CCCCCCICCT TATTCITICCT CATCACCTAC TGTTCCTCCT ACCAAGCCTC CACCAATTCC	600
5	AC	602
	(2) INFORMATION FOR SEQ ID NO:924:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LFNGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1574UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:924:	
30	CATCAAAAGC GTGAAGCTGG AGCGTAATGA GGAGCAGCCA GTTGTTTCGA TGGACTGGGA	60
	CCAGCTGTAC GACGTGTCTT CGAACATAAT GGAAGAATTT ACAAAGGAAA TOGACGAAAT	120
35	AGTGGCAGAG CTCAACCAGT CGTTCAAGGT ATGTAGCACG ATGAACACGC AGGGCCGGCG	180
	OGTTACTAAC OCCATOGGIG CACAAGCAAT TGCTTTGOCA GGAGGCGGGG TTTACCGTCG	240
40	ACTOSCACAG AGSCGCCACC CGGTTCGGGG CTGCGGAAAG CTGCATGAAG AGCAAAGAGA	300
	COCACCTOGA ACAGAAGOGG COGGAGCTCA ATOCATCOGC GOGCATCATC AAGAGCACGC	360
45	TOGAAAATTT GACGCAGGGA TAGTCCCCGC CGGCATCCGT CATGCAATGC CTTGCTCAAC	420
	ATTACATOGA TOOGTATTTC TOOCTATGIA CAAACATAAT TTACGCGAAT TTACCTTTCT	480
50	TOCAMOSCOT GROCTOGGIG TOTGCGCCAT CGGGGGCTTC AGITTCACTC TCCGAGACAC	540
	COOCGTCTGA GTCAAACTCC TCCGCCACGT CATCGTCTTC CCACTCCGCC TGCAAAATGCT	600
55	OSTOCACAGA CTCATOGTOC TCTGCAGCAG AACCATGITA ACGTOCTCAT CTCGCTGTCA	660

	GAACCAACOG CIGITIGIAG OCOCIOCIGA AICICITITCT CITICGITITT GACGCGGACG	720
5	TT	722
	(2) INFORMATION FOR SEQ ID NO:925:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 589 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1575RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:925:	
30	GATCCAGTAA ACTICAGCIC ATCGTGAGCA ACCGACGTCA CCCCACCACG CGCAGGGCAT	60
	ACTOCOGTICG AAATCACCTIG AGTATATOCA GTACTCTTOG AACCATOGTIG AGCAACCGAC	120
35	TOCACCICAC CACGOGCAGG TGAAAGTCCG GTGGATATCA CCTGAGTAGG TGCAGGCGAA	180
	CTGCCTGCGG AAATCACATC ACTATCAGCA GGTGAAACTC CAGTGGAAAT CGCCTGAGTA	240
40	CGTGCAGTAG GCCTCGACTC ATTGTGGGCG ACCCATGTCA CCTCACCCCG CGCAGGCGAA	300
	CTGCCTGCTG AAATCGCATC ACCACGCGCA GGCGAGACTC CAGTGCAAAT CACCTGAGTA	360
45	CGIGCAGOG AACTGOCTIGC GCAAATGOCA TGACGACGOG CAGGGGAGAC TCCGGTIGGAT	420
	ATCACCIGAG TOCGTOCAGI ACOCCTOGAC TCATTGTOGG CGACCGATGT CACCTCACCC	480
50	COCCAGCOC ACCITICCACI GGAAATCACA TOACCACGOC CAGGOCGAACT GOCTGTGGAA	540
	ATCACCTGAG TACTITOCAGI AGGCCACGAC CCANCGTGGG CAACTGACT	589
55	(2) INFORMATION FOR SEQ ID NO:926:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 684 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) OPGANISM: PAG1575UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:926:	
2 0	GATCAAATAT CAACIAAGGC ACTAGTTTTT GGTGTAGCTG CTCAAGCATC ACCGGATGCT	60
25	CAGAAGOGIG TAATTAACCT ACAATCTOGG ACTTCACCAC OCAAATCIGA AACACATTOG	120
	CATATACOCC ACAACOCTIC TAGCGIGTAT CAGTCOGAAA CAACAKATAA TATAACTAAA	180
3 0	GATACCECCA TGTTTTCTCC AGTCAAGTCA GCCTTTCCCC ATATACAACA GAAAACCATA	240
30	TCABCAGGCT CTGAACTTGA TGACACTGAC TTTCAGAGAA CACAAACTAC CAGCACAGGC	300
25	CCACTICCAA CITCAAGOCA ATAIGACICT GCCCCTGTGA CAGTTCATGG AGGACTTGAT	360
35	ATTICICCAA GACCACCITC CICTAGCICC ACAGATTICG ACGAGIATCC AACTGGIACA	420
40	ATAACAGAGT CACACAGAGG GOCTTATAAC GTTAGOCAAC TTOCOGAAAA TAATGGGAAC	480
40	TCASCTISCCA CTOSTGTCAT TAAGAGAAAC AGTTCTGTTC TCAGCTCGCC TGGAAGOGTG	540
	ACCACCACCC CAATGGTTAA TCRAGCTACA GTACTCAGGG CCTCGCCGGG AGCGGTTAAA	600
45	TEAACCGAGA AACAGCATAG TCCCCCCATCA TCTTCAGATA TTTCCACAGC CAATAAAACA	660
	CATTOGAATT CTATTGATOT AAAC	684
50	(2) INFORMATION FOR SEQ ID NO:927:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 732 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1576RP	
15		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:927:	
	GATCTTGTTG AGAACACTCA ACATOGGCGT AATTGCAGAG CCCCCGGTGA CCATACCGAT	60
20	THICHIGIAC GCATTOGICA CATAGOTGAA COGROCTAÇA GGACOTTIGA ATTOCACAGI	120
	TIGOCCIGOC IGIAGOCCAG CAAACCATIT GGATACCITA COGICGACAT AAGATITGAC	180
25	AATGATATOG AAATGGCCCT CGGCAAATTT GITGGAGATA GGCGTGTAGT AACGCACTTC	240
	TICTACACCA TOCAGCATCA COTTOGCAGO TAAATGAAAG COAGTAGGTA TATCAACAGT	300
30	TTCCACOCTT GAACOGAGCT TGAATCIGTA TATCGCAGCA TTTTTGCTTA GAACGATCCG	360
	TICTICCAAT TCTAATGGCG TCCACTCATT TGGAAGAATT GAAGTCCTGC TICTGTATGC	420
35	TAGTACCACG COTOCACCTA CAAACATTOC CAAACCTAGA ATOCCTAGAA COTACCATOC	480
	GITCOCCOCT GACCAGOCGA TAACAAGAAC GCCCAATGTA AAGATGCCOC TGGGGGATGAA	540
40	GATCCCATCA ATGGGATCAT CCAATATCTC CATACCTCTG CGFTCGGTCA TACTAATATT	600
	TIGAAAGCIC GICGIAGCIA TOGICIAGIA AGGATGAGAC COGITAATAT ATGCITCCIC	660
45	CTAGITCTAT AAGCACGGAC TCTTTGCAAC TGGTGAAGTA TCGTCTAACG GTCATCATGC	720
	ATCTOCCGAA AA	732
50	(2) INFORMATION FOR SEQ ID NO:928:	
5 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1576UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:928:	
	GATICAGGOOG GACGGGTACT TIGCAGGAAGG CCTICACGAAA COCAAGGGGG GCCAGGAGGG	60
20	CITCTOGACG TITTTCAACG AGACGGCCTC GGGCAAGITIC GIGCCGCCGC CGGIGIACGT	120
	GCACTTGCAG CCCAACGTCA TCCACCAGGT GCGCACGGGC GCGTACCGCG AGTTGTTCCA	180
25	CCCCCACCAC TICATCACCC CAAACCACCA CCCCCCAAC AACTACCCCC GTGCCCACTA	240
20	CACCOTTOGGG COCCACCTCT TOGGACGATTAT CCTAGGACCCC ATCCCCAAGA TCTCCCCACCA	300
30	GIGOGACOGG CICCAGOGCT TOCTICTICAC GCACTOGCTT GGCGGTGGTA CGGGCTCCGG	360
35	CTTGGGGTCG CTGCTTTTGG AGCAGCTTTC TATGGACTAC GGCAAGAAAT GGAAATTGGA	420
33	GTTTGCCGTG TATCCCGCGC CACAGGTGTC CACCTCGGTC GTGGAGCCAT ACAACACCGT	480
40	GTTGACCACC CACACCACAT TGGAGCATGC CGACTGTACG TTCATGGTGG ACAACGAGGC	540
40	CATCHACGAG ATGTGCAAGA AGAACTTGGA CATCTGGAGA CCTAGCTTTG CGAACTTGAA	600
45	CAACTIGATO GOCCAGOTOG TOTOCTOGGT GACOGOGTCA TIGOGTTIOG ACGGCTOCTT	660
45	CAACCTOCAC TIGAACCACT CCACACCAAC TIGGTGOCKT ATCCAAGAAT CCACTTCCCA	720
50	TICC	724
50	(2) INFORMATION FOR SEQ ID NO:929:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 686 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDHINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1577RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:929:	
20	GATCCGITTA GAGAAAAACG GIAGCCCCGT GAAATACGCA TITGAGTGCG CAGAGCCCCC	60
	CGAGCCGTCC GAAAGGTAGA TTTTGTCCAG TGGGAAGTTG ACTCGTTTGC TTATTTCGAC	120
25	AATOGACGIC TICAGCICCC CGICTICCAA CGGGGIGAGC TIGITGAATA AAGCIGIAAA	180
	AACTOOCTGA AGAGCAGTCA GCACCAGATA GAAGAACAGC ATCAGGATAG AGACGTAGCT	240
3 0	CACCAACCCA GICCACAACT TITICAATTAC CITICAACACC GCATACCCIG CACCAGICCT	300
	AATCATGGAG GAGATCATAA ACACTITIAG CIGGICCGIT AGCCATAGCT TGACCGIGGA	360
35	CTTGTTGAAC CCGAATTTTT CCTCGACCAC AAAGTTGTAG TAATACCTCC CAAACAACCC	420
	CTGCCACCAG TICAGCTGTA GGTAGACGAT CAAAAAGTAC ACCGACTGCG ACATGGTCGA	480
40	TACTOSCACC ASCATGSCGG GCATGCGCTG ACCTACCGCC ACTOCTAGGT TCCACATCGG	540
	TOSCASCCAG TOGIACITAA TCATTACCAG ATTTAGTCCC AGGAACACCA GATCICTAAC	600
45	CATACOGIAG CGTIACITOG CCCCCCCCTA CCCCTCCGTC TITTCCATTG TITCTTTATC	660
	AATAACGCCC TOCAGTTCGC TGGGTA	686
50	(2) INFORMATION FOR SEQ ID NO:930:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
55	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1577UP	
10		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:930:	
15	CATCTTCGAC ACTATGTAGG CCGCGTAGAT GAGCAACATT ACCACGCAGT CCAGGACGGA	60
20	CACAGOGITIC ATCAGGCATA CGITAGCOGAT AATGCAGACG GOCAGCATOG CAAACAGITAG	120
	GICCACCATG ATOGAATOOC OCTOCOCOOC OCTAAGATTT ACOCACOCAG ACCTCATCAC	180
25	CATAAATATC GOGCOCTIGTA CCACACAGAT GATAACGCOG CAGGOGCOCCA GCACCTICACC	240
	CACAGACAAG GOOGGOGCAT TOTTGGCCGC GTTCCACGAC ATCAGACTGG AGAACAAGTC	300
30	GCCCGACGAA TICCACCATG CCAGTACGAT GCCTCCCAGA ATCCCCTTGT GCCCCCCGTT	360
	COSTIGUCIC GICAAGGICA CCACIATUGG ACATAAATAA TCAGAAGGGG AAACGCCCAG	420
35	CAACACAAAA CACACGCTCA GATGTAGAAC OGTCAGCACC ACGAACCCAG GGATAGCTTG	480
	TICHICICH ATAGATACAC TOGATGIGIG ATCCGIGCCC ATGIACITGG TOCATGGTCC	540
40	ATCCTIGCAC TCTGCCTTTC CAGGTACTTG GTAATAGTAG TGGTAGCCAC CGCAACACTG	600
	GICAAAAAGC ACACCIRAAA CCICAATATG TAAGGCGIGC GAATGGTAGA TGCGITATTT	660
45	AMMATOCAGT OCTTGAGATG AMCAGATAGA CTOGTGCCC	699
	(2) INFORMATION FOR SEQ ID NO:931:	
5 0	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 672 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genamic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1578RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:931:	
15	CATCATCCIG CIGCGAGNG AAGICATCIT GCGATTQCIT CATGCATAGG AGITGGNAG	60
	CACCAAACAT AGGATTCATT CTCAAGTCCA CCTGCGTTAA CCGTTCTGTC CTATACTTTA	120
20	AGTAGROCAT GAACTGTCTT GTAGAGRGAG OCAGGTTATT AAAATTAAAC CTGTGGGAAC	180
	TATCCCGGIC TAGTCCGATG AGATTATCCG TAATCTTATT CACGACACCC CAGTCCTCGT	240
25	TOGATAGAOG CIGOCTACOC GCAGCCICAT TOCGCAACTC CITATOGATA TOTATTOCAA	300
	GGATCTCGIC CAGGAGAATG CTACCATTIT TATOGITCGT AATGAACITG CCTCTACATC	360
30	GASCAAASCA TAGGIGITTA AIGIGGAIAT COSCIAGAIC GAACCCAGAC TCATOSCOGA	420
	CTTTCTCTGT ATCTAGCCCA AAACCATGCA TTAGCAGCTT CAAGACAATC GCCACAAGCT	480
35	COCATTGITC COATGICCIG CAACCAACCT TIACCACATA TOCCATTOCG TCATCCCCCC	540
	CATGITCAAA GITTIGCAGC ATTAGCACGC AGCTAGTGGA TOGGGTGAAC AGCATCCTAG	600
40	TAAGGACCOC GACGAACTICA ACCITICTIGTIG CTACAATTATIC ATCACTIGGAG AAAAAACCTICA	660
	GAAGTTCCCCC CC	672
45	(2) INFORMATION FOR SEQ ID NO:932:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 737 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1578UP

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(xci)	SEQUENCE	DESCRIPTION:	SEQ	\mathbf{m}	NO:932:
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Galcillic	IGGITCITIT	CCITIMANCA	GAATAATAAT	TGAACAGGTA	CCGIATIATC	60
GCCGCATGCT	AAGTGCACCT	TTGACCGAGA	CACTITAGIG	ATATTTATT	TOSTAGTGIG	120
CTOGTATACG	TOGGCCACGA	CITTCTTGCC	ATTAATCTCG	TCCTTGGGGA	AGCCGTCCTG	180
GTAGCATCCT	AACGCACTCA	TTAATOCCAA	TCATCOCCOC	TTGATCOCCT	CACGCCCATC	240
CGAAACAACA	CAGACACATA	TOOGITTOCA	00CATC0000G	CCCCAAATAT	CAGAACCCTT	300
CCCTCCACTG	ATTTTTAAAA	TGPTGTCCAT	GACGCCTTTT	AATGTCCGTG	CCAATAATAT	360
GICGTTTCG	TTGTACATOG	TTATCACGAT	CATGATTICT	GTCCTACCCG	GEACAGCGEA	420
TTTTAATTGT	CTCACGGTAA	AGTTCTTTAG	CTGAAACTCA	GCTGGCTCAC	AGGIGACAGC	480
CTGATATOGC	ATGAATTTGT	ATTOGTTOGT	GAAGTAATCT	TCTCTCATGC	CACGIGOGIA	540
CTGOGACACT	AGCTGTTCAC	TGACTGGACA	ATCAAAGATA	AAGITTOCTC	GATATAGCTT	600
GAACTITOGT	AATACAATGC	GATTTTTAGG	CTGTTTCGAC	TOCOGTAAAC	CACTCAGAAG	660
CCGTTCTGAG	CTGAGATOGC	TGCAGTCGCC	AGAACCTTCG	CAACCOCACT	ATGCCCATTA	720
GGGGCTACGC	GAGAGAT					737

(2) INFORMATION FOR SEQ ID NO:933:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 663 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEINESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1579RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:933:	
10	CATOGAAATA COACTGATOG ACOGOGGIGO CICOCTTIGO AGCIGOTOGG AGAGOGGGTO	60
	TOCGACATAC COCCCAGACC ATGCCTTTTC CAACACCATC TTCTCGTTACC GTTCGGCAAG	120
15	TGACCCTACT ATACTTATGA TAATGACCTT CTTGTCCTTC ACAGTGCCCT CTGTTTCCTT	180
	CTTCAGGIAA AGGIGCGATT CTCGGCCAGG CTCGTAGTAG CCACGGACGC CAGACGCAAT	240
20	CCCCCTCCTC CACCCCATCC GATGCAACTA CTCCACCCCA CACTGCCCCC GCACAACCAC	300
25	CGAGITGITC ACGCCGACCA CGIACICCIA CTGGTGCTCC AGCGGACACA CCTGGAGCGG	360
23	ATACTCCTTC AGCGGCAACT GGCAGTTCTG TGACCGGGTG TTCGCAACGC TCAGCTGGCC	420
30	CTOGACCAGO COCCAGACOC COGCCATGTC TOCCATGTCC GGCAGGTACT COGTGTGCCA	480
50	GCACCAGGAG TCATTTCCCC GCGCTACCGC CTGCAGCGCC TCCTGCTCCA GCGTATGCAC	540
35	CTGCTTCGCA GTCAGCTGAT GGTACTCCGT GCTCTGGTCG ATCAGCAGCC CGTCCTCCGG	600
	GGICIGCCAG ANCOGCATICC ATCCCACCAC GCITTIGIAGA AACCAGGICG TGGGGGCCCT	660
	GCA	6 63
40	(2) INFORMATION FOR SEQ ID NO:934:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
55	(A) ORGANISM: PAG1579UP	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:934;	
5	CATCOCACGG ACCOCGAGAC GAGTICCTCT GGITCTGTOG ATTGGCCGATG GTAGGCCGCC	60
	CTGTTGCACG TGACCTGGGG ACAGCAGACT TGGGGTCAAA ATCACCCTTA GCCTCAGCTG	120
10	TGATGACATC AGCCAAAACG OCCGTCGGTA AACACCTTCC GACGCGTTCG TMGACTTGAG	180
	CATCAGITTA COGIGCITAC CUTICCOGIG COCCITITICG AAGGACICOC GGAGOGICIC	240
15	AATAICTIGT GAGAGCIGIT CCAGCGAGAT ACCCTCTTCT GGAACGTAGG AAACCTGTGC	300
	GOOCACOGOC AAGGCAGCAT GOGFTGCCAG ATAGCCTGAG TTACCACCCT GGACATOGAC	360
20	GACAAAGACC CGCGCTCTTG TGGACGCTGC CGACTGCTTC ACAACATCAC AGTACTCCAT	420
25	TAGGGCATTC AGAGCTGTGT CTGAACCCGAG CGAATACTCA CTGCCCGGGGA CGTTATTCGA	480
20	AAGTGTTOCT GGAATGAGTA CCATTGGTAT TCTGAAAGCT GGGTAGTTCT CACGGGCCCCG	540
30	CTCCAATTGA TGCAAGGAGA CGAAGGCTCG AACCCACCAA CAATAACCAA GCCGTCAAAC	600
	TIGIACITIT GGAAGIAGIA GGCAATCATG CCAATGICTG CATCTTCTGG GACAGTTCTG	6 6 0
35	TTGGTTCCCA ACTOGGAACA COGOGAGATT GCCAGCCAAG CATATCTTTC CAGTTCAACG	720
	(2) INFORMATION FOR SEQ ID NO:935:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1580RP

(xi)	SEQUENCE	DESCRIPTION:	SEO	\mathbf{m}	NO:935:
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5	GATCCGIGIC GACAAGITGG TCACGTATAT ATGGCGCGIG TTCGAGCGCG TCTGCGIGIA	60
	CCCGCCGAAC CAGCAGCGCT GCCATCTCGA AGACATCATG CTCTTGCGTG TGTACTGCGG	120
10	CGAGGCGCGC GGGCACCCCC TCTTGCTCAT GGCCATCGTT CAGGCGGTGG CGGCACGCTA	180
	COCCOCTOCTICT COCCOCACCACCT ATTICATION ATTICACCOCA ACTITICOCCCC	240
15	COCACACTCA TACTICATGA TCCCOCTOCG ACOCAACOCA AACCCCCCCA TCTTCACGCG	300
	GCGGCGCTTG CTCGACACTA TGCGGCACAC AATACCCCAAC ATTGCCGACC CGCGGAGCCT	360
20	GOODCTICOCC COGTITCCTICA CTCCCGCTICAC GAAGCCGCCCG GGTIGCTIGAGA AAATICTTICAA	420
	AGACTIGGTOC ATCTACTIGGG ACAAATCCAT ATGGCGGACG ATCCCTGATC ACTGGCCCAA	480
25	TESCATTICTE COCTACCTCC COCACTCCTE CACOCCCATE GACGAATCCA TCTTTGAGTA	540
	TITICATOGIC TATTOGAAAA COOCAACACC AAACCACTOC ACGAACAACA TITTICCACAC	600
30	CONTENTED ANGENITIES ANACESTED SCHOOLS ANGEST ANGESSES COCATOCACT	660
	THEICCATTE CCCCCACCAC CICATCCACT CCATTATOGA CATGICITTIC CCCACTCC	718
35	(2) INFORMATION FOR SEQ ID NO:936:	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 705 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
- 50 (A) ORGANISM: PAG1580UP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:936:	
5	GATCCTTTTC ACCAACAGCT GTCTGGGGCCA GCTGCGGCCT GGGATGAACT ACAACGAGGC	60
	AGTGAAAGCG CTGACGAACC TGGCGCTGGA CAGCTTTACA CTGCCGGGGG ACGGTGGGGT	120
10	TTCCGCTGAA CAACGTGTAC TCTGTGCCGG TAGAAGACGG TGCTCAGATG GAGCTGCTGA	180
	AGGGETACCT GCAGCAGTTG CGGCAGGAGC TGGCCACGGG GCTGCTGGAC GGTGTGTATG	240
15	GGGGGAAAA GGCACAGCCC TCGAAGTTCT GGCTGGCCTT CACAAGGGCC AAGTTTATGA	300
	ACAAGGOOCT GIVAGGOCGAA ATAGGTACGI AGCTUGCOGC GCCAGGAAGT ATTTACAAAG	360
20	TIGOCIGIAT COCTACGAGG TITTGGTGGC GTGTGCCTTG TTGCAGCGCA CGAGGAGTTC	420
	AACGGCGGAA GCTCGGAGCT GTTCCGCCGTC TTTCACCGATC GCGTTCACGT CAATGCTGAG	480
25	GTCGGTGTTT TTGGCGCGGA AGCCTTGCAT CCGCGGCTGC AGGTCTGTCA GCGCCTGGAG	540
20	GACACGCICA TAGICIOCAT CTTCTTTCAC GOGCICITTG TATGTTTGGA AGGACTGAAC	600
3 0	GATGICITCG ATACCGOOCT CGACTCTGCT GATCATCTCG ATGCCCTGGC GCAACAACTG	660
	ATCGCGGTCG CTGTTGGCGT CGCGTCCCTA ATCATCTGCT GCATT	705
35	(2) INFORMATION FOR SEQ ID NO:937:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 665 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1581RP	
55		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:937;

1189

55

	GATCITAATT TAAAATTITA ATTAACTATT TATAATTITAG AAATATATAA TCTAGAGATA	60
5	TATAATUTTA AAATCATAGG TAAAAATACT TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATTIG TGGCATCITA	180
10	ATTITIATTA TITAATIGAT TATTATCIAT TITAACATAAA ACATTITAAA ATGITATAAA	240
	ATAAATAGA AATTACTTAT AGAATATITA TIAAATAGTA TITTAATTITAA TITTAATATT	300
15	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGTTTA TTAATATTAA GIGATATATA	360
	ATTIAATTIA TATAAATTAT TTAATTIACT TCATTGATAT ATATAATTAT TAAATGIACC	420
20	TITICATAATA TITATTITIA TIAGICIAGI AATATTICIA TITAATAGIC TACCCITTAA	480
	TIOGATATTA CIACCIACTA AATATTIACC TAATAATATA TIATTAAGAA TACTIAAATC	540
25	TAATAATTEA TIAICIAAAG TATATAAAUT AATTAAAICE TITUTAITAT TATICIAAAT	600
	TATTATTAAT TAGTAAATTA TATTTATTTA TITTATTAAC ATAATTITTG ATAATAATAT	660
3 0	ATCAT	665
	(2) INFORMATION FOR SEQ ID NO:938:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 732 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1581UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:938:	
5 <i>5</i>	CATCAATTAA TAAATOGTIT AACTAATAAA GITAATAATA AATOTATTAA TIATATAAAA	60

CTACCIGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
ATTGAGTTTA TAPTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGITTAATTG	240
GUAAAACATA TGUUTTAGGG ACATATATCT TCAGUTCAAA ACUGAATATC TACATATUAT	300
ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATGCTGA AAGCATTAGG	360
GGIGIGIACC TTACCICTCT AATTAAAGIT ATAAAATTAT CTTAACTAAT AAAAATAATT	420
AATTAAATA ATAAATAATT AATTAAATTT AAAAAGA ATTAAATTAA TAAATAAA	480
GITATATITA AATAGATCAA AATITCAACA ATITCCATIT CATITAGTAC TACCATCACC	540
ATGACCAATT GITACATCAT TEAGITTATT AGGITTACTA TTAACTTEAG CITTTACTAT	600
ACATOGUATT ATTOGUAATA TITATCCTTT ATTATUATCT TEATUAGUAG TITTATUACT	660
AATAACTITA TGATTTAGAG ATATTGIWGC TGAACTTACT TATTTAGGIG ATCATACTTT	720
aactgtaaga aa	732
(2) INFORMATION FOR SEQ ID NO:939:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 694 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEINESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: PAG1582RP	
(xa) SEQUENCE DESCRIPTION: SEQ ID NO:939;	
(VI) SPROMER PERCENTAGE SPR ID MO1833:	
GATCTCAACA COGTOGTTOG AGAAGTGTOC AACACACGAG TACGTAGTAC CCAAATCAAT	60

	THE TALL THE TOTAL TA GAMALGAM TUTCTEGITT TUTCHTACC	120
5	GOGAGAAATA CCAATUUTUA TAACOOTIACG TAAGOCCAGA GOTACAAAGC TACTCCAATC	180
	TGAAGCTACA CACGCCCAAC CCTTTTATAC AATTTCAATT TTTTCTCTCC CAAACGAACA	240
10	TOOCAGATAG TAAGAGTCTT CGAGCCCAAT GCCTGTTCGG TTTTTTTTTT	300
	TTCTACCATA ACGTATGTOG COGTTGAAAA CTGATCAAAC GGGTCTOGAA GATCTTAGAA	360
15	TAGAGGCTCC GACAGAAAGG GGGAGGCCGA TTCAAAAAAG ACCGCATGAG CCTCACTCGT	420
	GCTTOGAGGC GGGAGAGCCC ATTAGGCTTCT TTCCCAGGGGC CACCGAGGGT TTCTGGAAAG	480
20	GAGCGAAAAC AGAGAATGAA CCGAGGGGT TCATCTGCAT CTTGCACTTG CCGTAGGCCC	540
	GTTTCAACTG AGCOGGAATG CGTGGATGCG AAACTIACCCC GTCCGCACCC ACCTCCCACT	600
25	TCCGTACCAC CGCACGCATG TTGGCCCATT TTCGTAGCGC GCCTTCATGA AAAGCGAGTA	660
	TAGAGCCAGC ACAATCCACG AGCGCGGGGG ACAA	694
30	(2) INFORMATION FOR SEQ ID NO:940:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 707 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
40		
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1582UP	
45		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:940:	
	CATCHTGITC TCCCCATCCA GATACTCGTC GAACCCCCAG TICATCTCGT CTACAATCGG	60
55	CTTCCACGAG TCGGTGTTAT CTATCGCGTC CCCGAAGCCC CGCGTGTCCA CCACCGTCAA	120

	CITCAACACC ACGCCGITCT CCTCGATCTC CGTCGTGACG GTCTCAATCT TCACCTTGTT	180
5	CTCCCCGTCC TTGCCCCGCG ACTCGTCCCCC GTCCTCACCG TCCTCAAGCT TCAACCCGTT	240
	CAACTOCTCC COCCIGTCCT CCTTCCCCCT CTATACCTCC TTCTTCAACA ACCTCTTCAT	300
10	CAAGGITGAC TICCCCAACC CCTIGGCGCC CACGCAGAGC AAATIGAGGI TGAACCCGCG	360
	CCSGATCGAC TTGCGATGCC ACTIGCTTGGG AAGGTTTGCG AACCCCACGT ACCCCCAGAT	420
15	CITECOGIEG AIGATCOSCA GETCTOSCIG GICIOSCAGC ACCTOSCOCA COSCCAGCIC	480
	COCACCCAGT CCCCTCCCCA CATTCTCCTT GTCGTCCCCA ACGTCCAACC CCATCTCCTC	540
20	CTCCTTCACG TICATGICCG AGCTTGIGIC CTTCGCCCTC GCCGTCCCGT TGCTCATTAG	600
	TECCCCCCC TECCICETTET CACCCCTCCC CCCGTCGTGG CACTGTTGGT GTTTGCCCAA	660
25	TOUTOUTGOG AGOCTIGTAGG TAACATOCTT GITTUTGATTT GGTAGTC	707
	(2) INFORMATION FOR SEQ ID NO:941:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1583RP	
45		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:941:	
50	GATCAATTAC CCTGGCGCCA ACCATATITG GATGAATATT TGCATTGTTG CCCATAGGGG	60
	TICCCICATC GIGIATGITA TAGACCITCA CGICTICATT AAAAGGGCAT GIGATGACTT	120
55	TOTTGCTGTC COCAGAGAAG GICAAACAAA TTACAGATIG TTCTGTACCG GCCAAAACTT	180

	MINISTERE GRASITOTTI MARMEGICAL MINICANIAL CITACATOS CIOCANSISTI	240
5	CAGTOGATOC ACTOOCCAAA TACCGACCAT CTGGTGAGAA TIGGAGGTAC CAGATTTCAT	300
	CTTTATTTTC CGAAAGAGTC TTCACATGAC TGAAATTGAA CATGCACATA GAGCCAACGT	360
10	TATCHTGAAG CAAGHTATAA GIOGHTITCT CICCAGAAGG GITTCCHICG TOGHTGTGAG	420
	CATCOTCOCT CAACCITAAC ACCICCCTOG ACCOCTOGAA CIGIATAGCC TGTTITAACA	480
15	ACCIPANTEMS CCITCOCCCCT CCAACCAAAT CATTOCCCTT CATATATTICT CAAATCTCAT	540
	CAAGOOCCAA TROCCOCCAG GCTGCCAGAG ACCCTCCCCA TATTTTTGTT GCCTCTGCGG	600
20	ATTOCOCAGO ACACOTOAAA ATAGTOOTOA CTOCAGAAGA OCTOTOTOGO GAGTOATAGO	660
	CCACTCTCCC TCGGGCTCCT CCACCATAGA TATGGTCTGT ACAGCCACAG CGAGTCC	717
25	(2) INFORMATION FOR SEQ ID NO:942:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1583UP	
40	CONTRACT. PRINCESOE	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:942:	
	CATOGACTOG AAGTACACOT CCAGOGACCG GTCAAGGCCC ATGTCCTGCA COCACTGCTC	60
50	GAAGGICITC ACGAGGTICT TGGGGATGGG GAGCATTGGT GTGCGGTCTG GGGGGGGCA	120
	COCTOCOGRAG COCTOACCOR ATTROCTTOT COCTOTOCTO ACCTORACACT TOCOCCOCTO	180
55	CCCCCCCCCCCCCCCCCCCCCAATIGG CTGCCCCCCCC CTGCCACGCC GTTCCTGCAA	240

	TCACATGATT CATGATTCCG CTTTTGGGGG GCATCACTGC GCAGCCGTTT TTGCTGCTTT	300
5	TAGOCTOCCT CACACCCTOG GCTGCCSTCTG GACGCAGGTC CCCGCCCGCT GTCCGCTGCG	360
	TOSCTOTACG TGTOSOGTGA COCCATTITIC TGGGACAGGG GCGACGCATG ACCACGAGCT	420
10	CGCAGGGTCC GCCGTTGACG ACAGCCCCCT AAAGGAGTTT CTTTTATTGG ACGCGGCCCC	480
	TCAAACACTA TATATGAGCA AAGGCAGGAT GGAAGGTAGG CTAAAGCAAG AAAAGACCTC	540
15	GACCAACGGT ATCGAAGTCT AAAATCTTAG CAGGTACCAG GATGTCTTTC GAAGATTTGC	600
	ACAAGOCOCA ACOCOOGAAA GIOGAGGAGG CAGTGGACGA AATATGTAAG GATTTOGAGG	660
20	TGACGGAGGA CAAACTCOGC GAGITGACGG GGIACTTCAT CGAATGITTIG GAACAG	716
	(2) INFORMATION FOR SEQ ID NO:943:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 677 base pairs	
30	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1584RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:943:	
45	GATCCAAAAA GCCTTCCGGG CGCGGGCACA TITIATCACAC CCGCTGTGCT TGACGGCCTC	60
	GACAATACAT CCTATGACAT CCCTAATCCC TCCTATGTTG TTCCGACCCG GCCCAAACGT	120
50	OCCAPORICT CGAAGGCTTC GCGCGCGAGC AAGAGTTCCT CGCCCCTTGA AGAGGAGGAG	180
	AAGCCATTIA AATGCCAAGA ATGCACCAAG GCCTTCCGCC GCAGCGAGCA CTTGAAGCGC	240
55	CATATACOCT CTGTGCACTC ATCGGATAGG CCGTTTCCGT GCACCTATTG TGATAAGAAG	300

	TICARCURA GULACARICI GIOGRAGIAT CICARGACAC ATCOCARGIA TURCGATATA	360
5	AAAGACACOC CACCAACCAC CAAGAAAGOC TGACTITICAC ACATCTATOC GAATACCOCA	420
	TOTTGCATTA AGAGATACAT ACAGCOCATA CAAGCTGACA CAACGTCCCG TAGGCCAACA	480
10	GAGGAGATGA TAAATACTAC ATACTCAATA TATCAATACC TCCTACTTTT GGTAATCATA	540
	TATAACIGIT TICTTICOCA CIGITCIGGI AACGITGICA TAGGITTCCC TGITGCIGCT	600
15	AGCTGGCCAG GATTCCCTTA ATGGATGAGG TCCGGGCGC AACCAGACAA AAGTTGCGCA	660
	OCTTAAGATA GITIGGAC	677
20	(2) INFORMATION FOR SEQ ID NO:944:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 706 hase pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1584UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:944:	
	CATCCCATTT TGTCTTCTTC CCCTACCCCG ACCCCCAGIA CACCATCCAG AATACATCTT	60
45	CACCACTAGE CITECCAAGT OCTCATTAGT TECCETCACA TECCTECCCCE TETACATGAC	120
	ACTGACACAC CATGITGTAT TCATATOGAA GCTGGAAGGC COCTGGATGC GCCCAAGGCT	180
50	CANTOCANTE CACOGRACITE CATOGGACTE GENTITIGGTE TECRASCITE GARACACTAR	240
	TATTOGGAAC CTGAATCATG GGGAGGIGGT GATCTTCCCC TCACCCATGA ACCCCAAGAA	300
55	AGTATACTOC AAGCOCATOC AGOGTAAGCA GTATGATACG GTGCGCACGC GGTATCCTTA	360

	TCCGAAGAGT ACCTGCGAAG TGCCAAAGTC GCACATATGG GTCGAGGGGG ACAATGTCAC	420
5	GCAGTOGGTG CACTOGAATC ACTTCGGGGC GATTTCGAGG GGGCTTGTGG TAAGOGAGGT	480
	GACACISCITC ATTATESCOCC CATOCACATG COCCOCAGAC CTGCACGAGG CCATGGGTCG	540
10	ACCCCCAGIT GITCCTTCAT GATTCCCCCGA CCCCCCGTAG GCCAACCTAC CCCTACGTGT	600
	ACATAGCTGA AAGACTAGAT ATTATATAAT GTOGAACAAC GTOCTOCACT GCOCCAGAAG	660
15	GATGGCTTAA GAATCGITGT CCTCCTCCTT GACGATCTCT GGGAAA	706
	(2) INFORMATION FOR SEQ ID NO:945:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1585RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:945:	
40	CATCCCCGTT GITGTCCACG TGTGATTCAA TATATACATA CTGCAAGTCT GTACATGTCC	60
	TCTATTATAT ATGGIGCTCA TGTTGCGCTT ACATTCTTTC TTTATACAGT TCATGTCCTT	120
45	COGREGIESC ATACCEAGIG ATGCCCOGICA TACCIOGTAA CCACAGITTE TATAATCATT	180
	CAGGCIGAAC IGAICAAIGG AGCIGCGITT GCCGAATTIG ACGCAGAGGI TIGIATACAC	240
50	ATTGATGTCC GCCCTCGTAA ACCCCTTGCT AAACGTGCAG AAGCAATTCT TCCGTTTGGA	300
	ACACGAAGIG CAAGGCITCA ATGCTATCAA CITATCCACA TGCTTCAGCA GCGTCAGTTC	360
55	CTITICICACE ACCECCICCE TCACCICCIC TOGAATCIGG CTAAGCCACT CCTITICCCAG	420

	CICARACACA IN IACCOGIG CONCAMBOAT CICGITGAAC GASCOTIGIGA COGAGGOGTIC	480
5	CTGGAACAGT ATCGTGATCG TGGCGTCACA CTTAATCTTC TTGGAGCGGC AGATGTCGCA	540
	OCTOGOCCC GTCCCCTGAC GCTTGTACTT CCACCCCGTG ATAACCGTTG CCTCCTGTAG	600
10	CAGCGAGITC GETGGCCAAC ACTGCCCTGC ACGTCCCCCG TTGGAAGCCC GAAGCAGATT	660
	CCGACATCAG COOCGACATC GACACOCCOC CCCCCCACTC TOOCGACCCC CCCTGT	716
15	(2) INFORMATION FOR SEQ ID NO:946:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 740 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI585UP	
30		
35	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:946:	
	GATCACTCTA COCCCACAG TICATTCACT CCACTGACCT GAATGTCACA CAGTCACCAT	60
40	TTTTCAACCT ATCACCCTCA TCCCCCACCA TCACTCCAAC CTTCCACCCT TTTAAATTTT	120
	CTACATTICG COCCAGAGIC TCATAGGAAA TAATCAATAC AGGCTIGACT ACATTACGGC	180
45	CCTGGGCAAT CGCCCACTGC CTGACGCACT GTGCAACGCA GCCGTTGGAA AGGGAACTTT	240
	TACGICCATC GATAGCCAGT GOCGAAAGGG CATCGGGTCC CAACCACTIC ACAATCTCAT	300
5 0	TAGCCCAGTT ATTAACCAGG GACGAAGGGC AGACAATGAT GCACTTTTCA ATTGTAGGAC	360
	CACCITICACA COCCIGOCOT ACTACOCTOC ACATTAACOC TATACATTCC ACCEITITAC	420
55	CTAGACCCAT TTCATCAGCC ATAATACACC CATAAGCCCC CCTATTIGAT TCTCGAGTCA	480

	TAGCTGCATT GOCATCCAAG ATCTCAGGCG AAGGGGTGGGCGTA AGAATCGGCG	540
5	TOGGOGTCTC CTCAAGCACC TOCACAACTA TTGGCTCACT ATCTTTACTA COCGGATCCT	600
	TACCAGIGOC ATOGICTIGO ACCITOGOCOG CIGOCAAGAG AGOCIGIGIA TOCAAAAAAT	66 0
10	COTTCATORC CAGACCAGIC ACACARCRET ACAGGAATOT TACCCCTTCC ACTTGATGAG	720
	GGCGTTAAAT CCGCGCCAGA	740
15	(2) INFORMATION FOR SEQ ID NO:947:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 702 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1586RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:947:	
	GATCAGGCGT AAGGCCAGGA TATGAACTAT GGAGACGTCT ATTTTAAACT CAATGGCATA	60
40	TAAACACCGC ATATTTCTTG TGGTTATGAT AACITCAATT ATCGAATCAG TCGCAGCGTA	120
	CASSSTIGGT CACACTITIAC CACCATATOC ASTIGITICAT COSCOCCACA CACCAAATAT	180
45	AACTGAGAAT TTAAGTTTCT CGAAGAGAGT ATGCAACGGG GGCTTGTCCA CTACGATTAA	240
	AAGAGCACCA GCTTTCTCAT GCCTTCAACT ATGTCAATAT AAATATATTG CAAAAGGCTT	300
50	AASCTCTGTA TIGAOCCCCG GAAATGITTIC TAGCAATGIA GCTCTCTCAT CTTCACATTA	360
	GGCTGCGAAT GTGCTGACCA ACTGCAAAAA CCCAGTCATA TCGTAAATAG TGATGATAGT	420
55	CAGCGCGATA TYTAACCGCG GGTGCAAAAA ATTGATTTGG CCCAGGATGG AACTGGGGGAC	480

	GITCIOCGIG TIMAGCAGAT GCCATAACCG ACTAGACCAC GAAACCAACC TTGAAGAACG	540
5	CACOCCOCCA AACCGACCAA CACAACCOCT GCAAACCACG TGCCTGACGA CTCTTTIAGGC	600
	GIGIOCIAGO GOSOCOCCA CICGIACTIA TITTATAAAC CITOCATOCA GGIOCGICCA	660
10	TATACAGGGC GATCCGCCCC ATCTGCAGCA GCCAGGAACG CA	702
	(2) INFORMATION FOR SEQ ID NO:948:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1586UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:948:	
<i>35</i>	GATCAACAAA GTCAAATCCA AAATTGTGCT GGGAGAGAAA AAGATTCCGC CATCATTGGG	60
	CCTTTTCTAT AGCCATCAAT TCAACAATOG GTTAAGCCAT TTGAAGCCTT CAGCCCTTTA	120
40	TCACCCTCAT CCTCACAAAC AACATGGCAC TGCTACCCAT CCAAGCAGCG GTAGTGTCCA	180
40	TOGGTATOCC ACTGATGATG ATATCATTGT CACAGGGGAG AACACCGTTT ACAGCCTAAG	240
45	CCAMCOGATT GCATATCATA TAGATGAGGA AGGAAACTAT TATTATGCTG GTATCGATCC	300
40	GITTACTGAT OCATTOGAAC AAGAGOCAGA TIGCTTATAT CATGAAAGIG AGGTAGAAAG	360
50	CGTAAATGTC AACAACTTGG ACCATCTTTC TTCCGATATC AACGAAGAAA ACATAGACCT	420
<i>5</i> 0	CGATGGTAAC ATAGAATTGT ACGATTCTGA CTTTGACCAC ACTTCCCTCG ACCAGGTCCC	480
	GAAGOCTACA GAAACAATOG AAAAATACAA TAATAAOCAA TACTACAAGA TGAACAOGT	540
55	TOTAL TOTAL AND	240

	AATCACTGAC TCATCAAATT GOCAGGGCAA CACTGTAGGG CTCTCATCTG ATTATGGAAC	600
5	AACTICCGIG CATGITGAAA ATGICTCIAA TGAGAATTCC TIGGGGTCAT CAGGCTACAA	660
	GGAGATATTC CTGAAAACTA TGATGACTAC CTTTACGAAG GGGACGAAGA TGATTTCGAT	720
10	(2) INFORMATION FOR SEQ ID NO:949:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 678 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1587RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:949:	
	GATCATOGAG AAGGAGCTOG AGGGCGTOGG CAITCOGGCTG AACAAGTCGC CTCCGGACAT	60
35	CATTGTGAAG AAGAAGGAGA AGGGCGGTTT ATGGATCAGG AAGACAGTGC GGCTGACACA	120
	TTTOGACCAC CACGOGATCC OCCOCGGTCAT GAGTGAGTAC COCCATCAACA GCGCGCACAT	180
40	TECCTTOCOG TECCACOCCA CACTTCACCA CCTCATTGAC GTCCTCCAGC CTCCCAGCAC	240
	OCCUTAÇATE COSSCILATOT ACCUTOCUCAA CAACATOCAC TOCCUCICAC TOCCAACACUT	300
45	GGAGCTGCTG TACCGGATTC CGAATGCTGT GCCTATATCT AGTGGACGGG AGTGGAACCT	360
	AGATGAGCTG CTCGAGGTCA TGTGGGATCG CCTGAACTTG GTGAGAGTTT ACACCAAGCC	420
50	CAAGGGGACC ATGCCCGACT TCAATGACCC GGTTGTGTTG CGGTCAGACC GTTGCAGAGT	480
	GCGGGATTTC TGTAACCAAA TCCACAAGTC TCTGGTTCAG GAGTTCCGGA ATGCTTTGGT	540
55	TTACOGTAGO AGTOTGAAAC ACCAGOCTOA GTACOTOGOT CTTOCACACA CTCTAGAGGA	600

	TGAAGACGIT GTGACAATTC TGAAGAAGIA ATGTCTTGGC ATTTATGCAT GGTTTCAATG	660
5	CACACGITCT COCOCIOC	678
	(2) INFORMATION FOR SEQ ID NO:950:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 702 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1587UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:950:	
30	GATOCTAATA AAAGCTITTIC TGCAATIGCT CTACCTACGC CTGGAAGGTC GCGTAGGGCA	60
	CACCITICAA ATAGATGIOC AOGAGATACG ACCIGOGIAT CACOCOCCIT AATIGATICI	120
35	THAGTOCAAA CCAGATAGCC ATCAGGITTC GCAGGITTGA AAGCCAACCG GGCTAGAACT	180
	AAGCACGGIG COCACCOCAC GCTTACCGAA CAGCCGCCIG TGCGCTCTGC TACTTCTGAT	240
40	COCATOCCTA TACACAACTT TICACAACTA ACTGIATOCA GOGGCATGIC AATAACACAG	300
	ACACCCICAT CCACCGAAAT TGGATACACT GCGTCGAAAG CCTTTAAACC CTCCAATACC	360
45	TOGTACAAGG CATTOGAAAT CGTTTOGTAT TCATOGTAGG TATAGGGGAG GCAAACCAGT	420
	TGGGGGCACA AGITCTTGGC TTTGGAGACC CACATGCCAT TTTGTATTCC ACATTCCCGA	480
50	GCAGCATAAT TACAGGAGGC AACGTCCGAA GATGAACCCC CATGACACAC TGCCAACGGT	540
	ACTICGOCCI TGCTTGGATA GCCCGCCTTG ATGCCTGAAA TAGTCGCAAA AAAGCAATCA	600
55	AAATCCACGT GGAAGACGTG TOCTGGTGGA GCCCGCAAAT CATTTAGCGC ACCTTCATTC	660

	ATCCCCACAT GCCTGTCCAG AAACTCTCCC GTACAGCCCC CT	702
5	(2) INFORMATION FOR SEQ ID NO:951:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 685 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1588RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:951:	
	GATUCTITIAG TITOCTOGGAG TITIGAGOCTA GAGGTOCCAG AAAAGTTACC ACAGGGATAA	60
30	CTOSCTTGTG GCAGTCAAGC GTTCATAGCG ACATTGCTTT TTGATTCTTC GATGTCCCCT	120
	CTTCCTATCA TACCGAAGCA GAATTCOGTA AGCGTTCCAT TGTTCACCCA CTAATAGCCA	180
35	ACCIGACCIG GGTTTAGACC GICGIGAGAC AGGTTAGITT TACCCTACIG ATGAATGITA	240
	TOSCANTAGE ANTENACET AGENCIAGAG GAACAGETICA TEOGGATAAT TOGETTETIGC	300
40	GOCTIGTICOGA CCGGGGCATTIC CCGCGAAGCT ACCATICCOCT GCATTIATICCC TGAACOCCTIC	360
	TAAGTCAGAA TOCATOCTAG AACOOGATGA TICITTTTCT COCACATIAT AGATGGATAC	420
45	GAATAAGGIG CITTTAGCAT CGCIGAACCA TAGCAGGCOG GCAACTGGIG TICAGAGGGA	480
	AAGGTCTGGG CGCGTGCCGG CGCATTGCAA TGTCATACTG CGCGAGAGTA AATCATTTGT	540
50	ACACGACTTA GATGTACAAC AGGGTATTGT AAGCAGTAGA GTAGCCTTGT TGTTACGATC	600
	TOCTGAGATT AAGOCTTOGT TGTCTGATTT GTTTTCTATT TOGAAGTCTG CAGGAGCAGG	660
55	CTTTGAAATA GAGTCTTATG TTATT	685

	(2) INFORMATION FOR SEQ ID NO:952:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 723 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1588UP	
20		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:952:	
<i>25</i>	GATCCCGTAC ACGAAGAAAA TCGGACGGGC CAACCAAACC CAAAGTTCAA CTACGAACTT	60
	TTTAACTOCA ACAACTITAA TATACOCTAT TOGAGCTOGA ATTACCOCOG CTGCTGOCAC	120
30	CAGACTIGOC CTOCAATIGI TOCTOGITAA GGIATTTACA TIGIACTOAT TOCAATTACA	180
	AGACCCCIAT COCCCCIGIA TOGITATTIA TIGICACIAC CICCCIGAAT TAGGATIGGG	240
35	TAATTTGCGC GCCTGCTGCC TTCCTTGCAT GTGGTAGCCG TTTCTCAGGC TCCCTCTCGG	300
	GAATOGAACC CITATICCCC GITACCCGIT GAAACCATGG TAGGCCACTA TCCTACCATC	360
40	GAAAGITIGAT AGGGCAGAAA TITIGAAIGAA CCATCGOCAG CACAAGGCCA TGCGAITICGA	420
	AAAGITATTA TGAATCATCA AAGAGICOGA AGACATTGAT TITTTATCTA ATAAATACAT	480
45	CTCTTCCAAA AGGICGAGAT TITTAAGCATG TATTAGCTCT AGAATTACCA CAGATTATCCA	540
	TGEAGEAAAG GAACTATCAA ATAAACGATA ACTGATTTAA TGAGCCATTC GCAGITTCAC	600
50	TGTATAAATT GCTTATACTT AGACATGCAT GGCTTAATCT TIGAGACAAC ATATGACTAC	660
	TGGCAGGATC AACCAGATAC TATCTTAAAG AACAACCGAA AATGCGCAAG CACACCACGG	720
55	GIC	723

55

(2) INFORMATION FOR SEQ ID NO:953:

5	(i) SEQUENCE CHARACTERISTICS:	
-	(A) LENGTH: 741 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1589RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:953:	
25	GATCATTCAA GCATATTTAT TAATTAGATG ACATTAAACT ATTAGACCTT GGTTTGGGTT	60
25	GCTGGACTTA GGGTTGTGGT AGTCCGTGGG TTATATATTT TTTGTAGACA GTCACCAACA	120
30	CACTIGATET ATTICTITICA GCTGTGTGCG ATAGGCTCGC ATTGGATGCG GCACTGCTCA	180
	THEOCATOCT GCCCCTCAGC AATAACCATA GCCGCCCCCC CTACAACACCC CAAAAACTAG	240
35	GTTAGCTTCA TCTTGTGATA TTATTCTGTG TTTAATTAAA TGGAACTTTA GTGCTCTGGT	300
	TCTCTGCCAT AGAGATCAGG ACCTTGGTTA GATATCGGTG CCCTTATATA CACTGCTGCC	360
40	AAGGATOGAT GGACTGTAGC CGAGCACCTT CCAACTCAAA AGATCOGACA TCAATGTATT	420
	ACTGAGAGCC AGTATACTTA COGCTTATCA CACTAAACCC CATAGCCATG GTTACGAAGA	480
45	TOCTGATCTA TCATCOCACA CASCTOSCCA CTGTAAACGG ACTTGAGGTG GGOGACAGAA	540
	GCCCACTACA GGATGAGCGT AAATCTCCAA CAGCTAGCAA CACATGCCAT TAITCTATAC	600
50	GAACAGTAAC GIGCTIGATA TTACAGAATA COGATTAGGT TTTTTCCTGC CAGACCAAAT	660
	OCTATIOGIC AAACICAAAT TIAGICAGOC TIACATTACC TOOGTACCIC GAAGGIAGCA	720
55	ATGITAGGCA CTCTGGCAGT A	741

	(2) INFORMATION FOR SEQ ID NO:954:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 696 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1589UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:954:	
25	CATCUTCUTG COCATTATUG CAGUAGOGGT AGGOGGGCAT AUGAAAUGAG AUGGCGCACG	60
	TOOTGOOCIT GAGCACCIGA AAAATGOCAG TAAAAAGAAA OGATOOCOGC AACAITTIGIT	120
30	CCAGIGACIT TIGAGOCAGA AGIIACAGOCT TCAGCCCCGC GCIGCTTIGC TGIGGAITCA	180
	GACCACCEET CETCAAGETE GTCGTACACT CECGTCACCT ATCCTCTCAC CCTCCAGTCC	240
35	AGGACAGACA TACCOCCCAC TATAGCAGOC CGATCACATA CATAAGTAAG AAAATTAGCC	300
	CCASTAGATT ATTISTOSOGG TCATOCAGTIS CTOCACCATT GOGTGATGTG GTGTTGCCGG	360
40	GIAGICIOCO ACCATOGIGA TACOCOGAGO COCCAGATOC AACOGGAGGI ATAAAAACTG	420
	GTAATGGGAC AAATGGGGG CGGCCCCGGC CGCCCCTTCC GCCCCCTTAA GAAGGCAACC	480
45	COSSCEPTE COCICCICCA TROCAGICTT TIGOCCICIT COGIGOCOCC TGIGCICCOC	540
	CENTIGERCO TITAGRECCIC TACORRORGE OCTUTOCCCC COSTICORST CTITICORSCT	600
50	GIACGEAGGE GETGCCCCTT TCCCATCCTT CCCGCTGTAC CCAGGCCGTC CTCCTTTCCG	660
	ATCCTTCGGG CIGIATGCCG GAAGAACACC CTTGGG	696
5 5	(2) INFORMATION FOR CRO ID NO.055.	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 640 base pairs	
5	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1590RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:955:	
20		
	CATCATAATG ATTTGTCTTA ATTCTTTTCT TAATTATTCA TTAAATAATT AATTAATATT	60
	TTATTAATAA AAAATATTKA KAKKKATGIT CGITTATGAT AAATTCIAAA ACTITIGSARC	120
25	The state of the s	120
	ACCAACTGAA CACAACTATG TAACGCCTGT AATTAATTAT AAATTATTAT AATTAAATAT	180
30	TCAAAAATG GIYAGATTIA TCGAGGATTA TCGAATTAAA TAACATGITC CACTGCTTAA	240
	GICTGIAACC GICTATIGIT TICATITITA TIATICCIAA CGIAGICAIC ACCCGAATA	300
35	CTTTAATTTT CATTTAATTT ATTCTTTAAT TAATAAAAA TAAATAGGTA TICATTGTTT	360
	ACTOCIAAAA CIACTOOOGT ATOGAATOOG ATTIOCIACT TIAGOOTIOG TITOCICAATG	420
	The contract of the contract o	420
40	TCAATTAATA TATAATITAA ATTITCACTT TATAAGICIT ATTCATATAA TTATTATTIC	480
	ATCITIACIT GAATAAITCI TAAAITAITIT TTAITAAITC TAATTATIAT TTIAAAITAAT	540
45	CATTOTACGA ACCOUTTAAG CCATTACGAT TAACGCTAAC CCCCTTTGTC TTACCGCAGC	600
45		000
	TOCTOSCACA ANTITIOGIT GOGATTATIT ANTIATATAT	640
	(2) INFORMATION FOR SEQ ID NO:956:	
50	(2) State Alica Tel (32) ID 140.950.	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
5 5	(B) TYPE: mucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1590UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:956:	
	GATCIATTAT TAGAGGIAAT ACATTTAAAC TAITATCTAA ATTCTTCTTC TTCTTATTTA	60
20	TICITAACIT TAICITATTA GETAAATTAG GIGAATGICA TGITGAAGIA CCATTIAITT	120
	TAATAGGICA AATITGIACA TITATITATT TIGCTTATIT CITAATCITA GIACCIATTA	180
25	TITCIATAAT TGAAAATATT TTATTTATT TACTAAATAA AAAATAATAA TTAAATAAT	240
	AATAATAATA TICATTAAAT ACTTIAATAT TAATATITIAT ATATTATACT TCTTTATCAT	300
30	TTATGAGGGT ACCTCATATT GCTGACTAGC AATAGGGGGG TGAACCCTAC GCACCTAAAT	360
	CATAACACIT TATCATTAAA TTATATACIA TATATTATAA GTAAATTATC AAACCATATA	420
35	TANGGIATAT ATATTANGAN AGITTGACIG AGIGGITTAN AGIGIAATAT TIGNOCTATT	480
	ATAAATCITT ATGATTICAT AGGITGGAAT CCTATAACIT TCGIATTAAA TAAITATTIA	540
40	AAATAATTAA AAATAGITAA TAATAATGAG AACATGATGT TGGTTCAGAT TAAGCCCTAA	600
	CHANGACAT TACACATOCG ANICAAACGI TAATATTATT AATTAATAGI ATTAATAAGI	660
45	GGIGTACTCG TGAGIAAAAA TTAAGAATAA TGAACTTAAA TTTAACTAAA TAT	713
	(2) INFORMATION FOR SEQ ID NO:957:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 720 base pairs (B) TYPE: nucleic acid	
55	(C) STRANDETNESS: single (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1591RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:957:	
15	GATCATAAGC ATCTTTAGCT CCACTATCCA TGTCTCAAAAT TTGCAGCTGA TAATAAAGTG	60
	GITGIGIGGC OGAGCGGTCT AAGGCGCCTG ATTCAAGTGT ATGCTTACAG CTGTTACAGT	120
20	TOGACACTCA GGTATOGTAA GATGCAGGAG TTOGAATCTC CTCGCAACCA ATTATTTTTT	180
	TTTTTTGGAG TTCCAATGCA ATATCAATTC TACTGCTGCG AAAAGGTCTC GTCAGCAGAT	240
25	AAAAGAATAT AGAATATGIA TATTTATATA CAAGAAGOGI TAACTGACIT TYTATTGITA	300
	TAATGCCATT CGAAGAGATA TOGCTTATTA ACAGCAATAC CCCCCTGCAG GTCCCCCGCCA	360
30	ACCOTTOTICC AGTGATGCAA AATATATACC TOOCATGATA AAGAAGGCCC TTCATATCAA	420
	ATGGCCCAGG CATTAATATC ACCGTTCCCG CGGCCTTCAA CCAAGTAGCC ATCTTTATAT	480
35	CTGACATATT CCACGGCAIT CTCACTATOC TCATCACCGC CGCAAAACCA ATGCTTCTTC	540
	TCTTGCCCGT TGTAAACCTT CACTGTACCT TCCTGGTTAG CGACAACTAT CITATTCAAG	600
40	TCAAACTGCA AACATGTCAC COOGTGTTCA TACGAAAATG TATCAGCCAA TGTACCGGTA	660
	CGTAGATCCC AGATCTAATG CTGTTATCCA AGGAACCAGT CACAAGGTTT AGAGAATCAA	720
4 5	(2) INFORMATION FOR SEQ ID NO:958:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 697 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEUNESS: single	
	(D) TOPOLOGY: linear	
55		

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAG1591UP	
10		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:958:	
	GATCCCCAAT GATCCCTCTC COOOCTACAA CATCGAGCAG CTCCCTAAAC AGTCCAAGAA	6
15		
	CAAGGACAGG CTGGTGGAAC TGCCTTATAC TGTGAAGGGG ATGGACCTCT CCATGAGGGG	120
	TATTCTUSCC CACATUSACT COCTUGUGAA GGACCTATTT OGTOGAAACA CGAAGAACTA	
20	MATERIAGE CALATOMET COCTOMONA GOACCIATTI COTOMAACA COMMAACIA	180
	CAACCTCTTC GACCOCCAGA COOGCAAGCA GCTCGTCACC GTAGAGCACC TGTGCTACTC	240
	The state of the s	24
	CCTACACCAG CACCIGITIG CCATGCTCGT GGAGATTACC GAGCGTGCCA TGGCACATGT	300
25		
	GAACTCTAAC CAGGIGTIGA TIGIOGGOGG TGTGGGGTGC AATGTGCGAC TGCAGCAGAT	360
30	GATGGCCAGT ATGTGCCAGA GCAGGGCCGA CGGCCAAGTT CATGCGACGG ACGAGCGCTT	420
30		
	CTGIATTGAC AACGGTGTCA TGATTGCACA GGCTGGTCTA CTTCAATATC GCATGGGGGA	480
	TATAGTAAAA GACTICICAG AGACCGITGI CACGCAGAGG TICCGGACIG ATGACGITTA	- 4
35	THE STATE OF THE S	540
	CGTATCGIGG CGCCACTAAG TGTGTACCAA GTTTAATAGA AGTTTTACCG CCCTAATATA	600
	OCTGTTANCC ATCAGTOOCC TOCGATCAGC TOGTOCAGAA CAGTAGTOOC COGTOOCTGT	660
40		
	CACCABOCTA COGGCCCCAGC GCCAGGTATC CTGTTCG	697
	(6)	
45	(2) INFORMATION FOR SEQ ID NO:959:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 669 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
<i>55</i>	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1592RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959:	
	60
GATCHSSANC TOSCHSACCT TOSCHCTCTG STUSCCISC MACTUSCISM TETUSCCEM	60
CTOGTOGTOC TIGACCATGT TOCCGTTOCA GCCAAAGTCC TICCGCAAGA CCTTOCAAGA	120
THE CONTRIBETOR CONTRIBUTION OF THE CONTRIBUTI	180
Tecchias dicharac recognist colonist colonisti intelector	100
TICICIOCIG GATACOGATG TOGATGIAGT TOGAGGAGGA GOCTIOGIGG TCOCCOGTIGT	240
	3.00
CASCAMAGES GEOGRAFICA FIGHESITTI COMMERCAT GEOGRAFICA GEOGRAFICA	300
TACAAGGTAA GCAGAGAAAA TTTTCAGCTG TCCTTTTAAA AGCGCGCACC TCGCGTCTTG	360
CAPACACAMATAC CAMINATAMAAN CAPACAMAMAN CAMAMAMANAN APPEARAMANAN ACCACAMAMANA	420
GARCATIC GUIATTIGI GARCATATI CHARCIGIA TAGIGHAA GUGAATTIC	421
TOTGCAATTG COOGTOTTTC TITTGGCGTTG GGACAACGCT TCCTTTCCAAA CACACTTTCC	480
PCCPPPCARCATE AMESINALCE CONTRIPRESCAND CARGEAUNIANCE CONCRUMENTAL MACCALISTANIANCE	540
ACTIVITIES OF STATE O	24(
AAGGCAGAGG CTGGGATTIAC AATGAGACTIC GTCACACATIA CTTCACCTAG CAGAACACTG	600
ርአአኔጢርያርጥ (ድልባጥያንጣጥ: እርያጥምምምም ነው	660
	000
GAGGAAAGA	669
(2) INFORMATION FOR SEC ID NO-960-	
(a) (a) (b) (a) (b) (b) (b) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c	
(i) SEQUENCE CHARACTERISTICS:	
(C) STRANDEINESS: single	
(D) TOPOLOGY: linear	
(II) MULBLULE TYPE: LINA (GENOMIC)	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: PAG1592UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:959: GRICAGGAC TOGGAGACCT TESCRICTURE GROCCCIRC AACROSARIA TOTOGCCCAT CROSTOGRIC TIGACCARGI TOGGGIRGA GCCAAAGRC TICGGCAAGA CCTICCAAGA TEGGCTIGAG GROGIACTOC TOGGGATGC CCTGCACGGI GGICAAGGIT TITCTGCGGT TICRUCGIG GRIACGARIG TEGARGINGT TOGAGGAGAA GCCTICGIGG TOGGGGIRGAG TACAAGGIAA GCAGAGAAA TITTCAGCIG TOCTTITAAA ACCGGGACC TOGGGIRGAG GAACGCATTC CCTITATITIG GAACCATAIT CTIAICTGIA TAGGIGITAA CCCCATITIC TCIGCAATIG CCCGGICTITC TITGGGGIIG GGACAACCCT TCCTITICAAA CACACTITICC ACCAACTCC TIGGITCCTT GGGIAACACT GTICTICTIC GCTGITTAIC TCCTGITAGT AACGCAGG CTGGGATTAC AATGAGACTC GTCCACACATA CTTCACCTAG CAGAACACTG CAAATCCCCT GCATTGCTIG ACCTGITTCT TCAATACATG ACACTTTGAGGACAC GAGGAAAGA (2) INFORMATION FOR SEQ ID NO:960: (3) SEQUENCE GRANCTERISTICS: (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid (C) STRAILEINESS: single (D) TOFOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:960:	
5	CATCCACTIC TTAACCTCCC COCCCCAAT CCTCATCCCT CCATATGTAA CCACAACTCC	60
10	TITGIATCCC AACAATIOCA OCTCAATIOC CATCAAGIAC GOGIATCCCC COCCTAGAGA	120
	ATGGCCAGIT ATAATTACCT CATAGICIGG ATGAGCATCA TGTACTGCCT TAAACGCCGA	180
15	ATAGATATCG TIGITACGCCA ACTTAAATTG CICATATACG CCCGAGTGTA CAAAGCAATC	240
	TOCCGTACAC TITICCAGCGC CACTAAGTGG CIGGTATGGA ACCCCAGGAA AAATGAAATC	300
2 0	CACAATOCAA TOTTGAATTG TTACOGACOO TOTAAATATG ATOGAAATOT GOTTAGOOGT	360
	GICATTEATT GCTATCATGC TATAACAGGA AAACTGCCCG CGGGTCATGT CCGGATCAAA	420
25	AACTITAACT ACTICACICC CTGTTGTTCC ATGTACCACT TACCGTCATG AAAAGGGTCA	480
	GIGAGIATTA AAGIATICAC GCAGIAAACG CIGITAGIGA GATAIGACAC ATATTICAAT	540
30	GTATCAAACA TCTCATCAGA GAAAGAATGG ACATGAAGGA AAAAACOC	588
	(2) INFORMATION FOR SEQ ID NO:961:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
••	(A) ORGANISM: PAG1593RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:961:	
	GATOGAAATA GACAACTOTG CAACOGTGTC CAAATGOCCC AGCAACTTCC AGGAATAAAC	60

	ALARGIAGAE CATAGORICO ARGIACOTAT OCTOCTOSCO TRACTATORO TRIOGRATICO	120
5	AAAGGACCAA ACGTGCTGCA AGACGGAGGG AGAATTCTTC AGAAGAATTA CATTATACAG	180
	CCTOCAACCT GTCACACCCA ACCTATCATC GTCCTCCTTT GTCCGGTTCTG CCAAAACACA	240
10	AGACCAGACC TCTTCAAGGG TCACTGCAAT TCGTTGTCTA AGGTCGCCAG TCACACGAAC	300
	AACCGCTTTT CTGGGCAAGT CAGGGAGTTT TATGGTACTA GTAACCGGGT TATTTCCCAC	360
15	TAGGAGCAAT GCATTCAAAT AAGCAGCCCA CAGTTCCCCAA TCAAATTCAC TGGCATTCCC	420
	ATCTOGAGGA ACATTATATT GGATTAACAG ACTTTTGTAC ATTTOCAATA TAGTAACGCA	480
20	TGTCCTCAAA AATAGOOCAT GTAGTGAAAT CCACTTAGOG GAGOOCATGT ATCCATCTTT	540
	GGTCAATATT GTTACAGTAT TAACGGCACT TATAATATCT TCCFTGGTAA ACCGCGTAAT	600
25	GITAAATACA GATGITAAAA TAGGATCATT GOCOCAATCT TOCACAACIT GIATAAATGA	660
	OCTOCCATGT CCATATATTT CITOCTACAA TITOOOCTAA AGITOCCAAT ATAGIACC	718
30	(2) INFORMATION FOR SEQ ID NO:962:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 652 base pairs	
35	(B) TYPE: nucleic acid	
55	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAG1593UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:962:	
50	CATOGATCTG TIGTAATTTG GACACCOOGA GCTGCAAGCA GOGTAACGTA TGAGCCGTGC	60
	TOTOGGCCT COCCATOCT ATACATAGOC TCATACCACA TCATCGGTTT COCCOCCTOG	120
5.6		

	TATAGCATUT GCAGCACAGG TUAGCCCGGA GCCACAGCAT AGACAGGUTC ACGAGGCTUG	180
5	CAGCAGAGGA AAAGATGGGC AAGCGATTTG ACTGGCAGGC GAGGGGGAGG CTGGTGCGCG	240
	CCCCCATTAT CCCCCCCTTCT TTCCCCTTCA ACCCCCACCACCTC CTCCACAACC	300
10	CGAACTACAC GAACCTGTAC CCGCGGGATG AGGTGTACAG CTTTGAGGAG ACGGCGGACG	360
	GEOGRAFICATE TOROGRAPIAC CARRIPORTICO ARCOGCIGOO GERGERCITIT ATCTOGRACOA	420
15	TGAAGGGETT CTGGGACAAG CTGCGGGAGG AGCAGGACGG CGTGGTGGTG TGCCGGAAGG	480
	CENTIGUECA CICCIATEAC GACGAAGICE TEACCITICC GITCCIGGAC CICCCCGACE	540
20	ACCORRAGEL CANDOCIACAE GLOCOCACA COCACCIOCOC CACCIOCAC CACCIOCIOC	600
	ATACCCACCA CTTGGGGGAC CTGCAGCTAT TCCGGCAGCT GCGGGGGACG GG	652
25	(2) INFORMATION FOR SEQ ID NO:963:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1594RP	
40	(A) OWNITED: PASITIONE	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:963:	
	GATCAAGACT GOOGAACTGC TAGTTTOCTG CTTCATGAGG TTTGGAATCT TGTCCACGAT	60
50	GCGGGGGTTC ACCAGGGGT TACGGGAACTC AAAGTCGTCA TTAAAGTCGC GAGCAAACCA	120
	GTACCACCAT TCTACAACAC TOGTAAGOOG CATGOCGITT TTCAAGOGTA TTGCGTTTGC	180
55	GAAGTTUTUA TOOGCAAAGA GOTOGOTAAG OGACTOTATO ATAAGCAGOT GOAGGACACA	240

	TITTACCACG ATGGTATICT TAATACITAC ACGGIGCCCA ATCTCCTCGC TCCTTTTCGT	300
5	COCCACGACT COCCTCATAG CCTTATCCTC TTCACTACTG CCCTTCCCCAA CATCCTCCCC	360
	CTICICCICG CGITGGGCAC GCICGACTIC CCGATCAACA TCACIGGCAC AIGATIGGGT	420
10	TICAGCAGIA COGITOGIGI TGATTGIGGC TACIGATGGC TITCTTOCAC GCTTCAATGG	480
	ATCTGACTCA AAAAGTTCTG TGGCAGTGGT AAGCTCAAAT AACCGGCAA ACGAGTTGGT	540
15	AACCIGCICC CAATGCGITG TCCCGAACIT GITGGIGITC TGGATAATCA AFTGCTGCAG	600
	ACAAGACCTA CCAATCCTGG CAATGGTGTC ATTTTCCTGA CAGATGCAAG AGACTAACAA	660
20	AACCAGGAAG CCATCCAACA TITCGITCAG TGAATCAAAG TAATGCGTAA CAGGGC	716
	(2) INFORMATION FOR SEQ ID NO:964:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 695 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1594UP	
	(W) CHIMITON: EMBIODAGE	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:964:	
45	GATCIGAATT TAAACGIGAG ATACCCCGTTT TICIGACAGA GATATATITC CCTATATCIC	60
	ACATGAAATC TICTACTOCA CATCAGAAGA GETATTITTT GAGTGTTATC CAACGACTAT	120
50	GCAATGACCC GAGAACCTTA ATTGAATTCT ACCTAAATTA TGACTGCGAC AGTAGTATCC	180
	CTANTATIGI CGAGACTGTT GIGGATTATT TGACGCGACT GGCGCTAACA CGIGTCGATA	240
55	TCACCOCATC ACAGOGIOCG TACTATGATG AACAAGTGAA CAAACCCCTT GCAACGIWTA	300

	ACCIATOGCA GITOCCITTA TIATCCATAT CTAATGTTAG CAGTATGTCT GITOCTCCAC	360
5	ASCAACTOCA ATTOCOSSIG GAATTIGOOC TIAAAATGAC CIOSITGAAA TGIATGITGG	420
	CCGTGCTAAG ATCACTAAAT TCTTGGGCCG ACAAGGCGAC GGCTCCAAAT GGCACATTAA	480
10	ACCACAATAG GGCATCTGTT GGCTCCAGTA CGATTGAAAG GAAGCACTCT TCCGCTTTTA	540
	OCTOTTICAG TOACACTATG AACACAACAC CTGTAGGAGA CCAGAATAGT GTCCAACAAT	600
15	COGANOCCAG TCAGGATATT GATGATCCCA CACAGITTGA AAAITTGAAG TIAAGGAAAA	660
	CAGAACTOCA AAAATGTATT COGTTATTCA ACTTC	695
20	(2) INFORMATION FOR SEQ ID NO:965:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 709 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1595RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:965:	
	GATCTTGCTG CTATCCAGAA ATGGGAAGTT CITAGACAAC GGGGAATTAA GCCCCTTTTC	60
45	CAATATTTTG AGGGICGTTT CATAGCTOGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT	120
	CIGITCATGI TOGCICATGA AAGGIGICIC TATCAAATCI AGCTCCATCA TOGCAGAGIA	180
50	GPTATTATCT TICTPCCAAG ACAGACGCAC ATGCCGCAAC TTGGTCAGGA TTACAGTAAA	240
	ATAATOGTAG AACCGCGGAC TCACAGAAGC GACGACCGCT CGAAATGAAG TCGGCCCGTA	300
55	GAAGATCGTG CGGCCCTGCT TCTCTATCAC AAGATGGAAC TGGGAAAGTC TGTTCACGGG	360

	GGACACCGIG CCCATAACGT GCITCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
5	CCCCCCCACC TCACTCTCAA CCTCCTCCAT CCCTCCCACC ACCTCCACAT TGGGCGTCGA	480
	GETGAACAGE TOCOGTGAGT TOACGTOGTG OGTAAACTCA GACAGGTACA CACACTOGGG	540
10	CAGGOCTICC CAATACATGI AGAGCACTIC GGCCGCGCCT TGITGCACTT GACGCGCCGC	600
	TTGCGGCAGA ACACGCACGA CTTGCTGACC TTGCGCCTGG TTTTCACAAT CTTGCCATCG	660
15	GACTOTOCCA TOCOGOCAGO TICAAGCAAA ATGAGTAGOO TATATTATT	70 9
	(2) INFORMATION FOR SEQ ID NO:966:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 731 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1595UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:966:	
40	GATCOCOGAC GIGGACCACT GCCCCCACAT GCCCCCCCCC ATCCTGGIGG TTTCTGCCCA	60
	CCGCAAGOGA CACGCCATOG ACGAGCOGTA TOCAGCAGAC GOTGCACACG TOGGACOTCT	120
45	TCAAGGAGCG CGTCGCGACG GTGGTGCCGC GGGGGTAAGGG AGAGATGGCG GGGGGGATGC	180
	CCCCCCCCA CTTCCCCACC TTTCCCCCCC TCACCATCCA CCACTCCAAC TCCTTTCACC	240
50	CCACCIGCCT GGACICATTT CCGCCGATCT TCTACATGAA CCACACTTCG CCCCGGATTG	300
	TCAAGCIGIG TCATCIGATC AACGAGTICI ACAACGAGAC CATCGIGGOG TACACGITIG	360
55	ACCCCCCCCC GAACCCCCCTG CTCTATTACT TOCCCCACAA CCACCCCCCCC CTCTCCCCCCT	420

	ACCICIOTO, COMMINOSC GOLARIGADO GOTOGRADAD CARGINOTOS ACCIANICARIO.	480
5	OCCCONCCTT COCCOCCAC TICCACCACT COCTGCCCCC CAACCTTCCC ACCCACCTCC	540
	ACGACGAATT GCACAGAAGA ATTGCCCCCC TCATCTTCAC GAAGGTCGGG CCAGGGCCCA	600
10	GEACACTAAA TOCTOOCTOA TOGACOOGAG ACGOOCCTGC COCGCTGACG CTATTCTCCT	660
	GCTATTTTCT GCTCTGTATA COCTGCCAGA CGCGCTATAT ATATAGAATA TGCATTGCGA	720
15	CGCTIACGCT T	731
	(2) INFORMATION FOR SEQ ID NO:967:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 672 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genemic)	
3 0	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1596RP	
35		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:967:	
40	CATOGACAAT CTGAGCGAAA TATTTAGCAC GACATGCTAC ATGGGCTCTA CGGTGATAGT	60
	ATGGGAGTGG AGCAACCGGC TGTCCATACT GGAGGCCAGG CGCCAGGCGC AGAGCATTCT	120
4 5	GGGGCGCCCG GTGTATGAGG ACGAGGACCA GGGGTACAAC TTTGCCGCCAT ATGCCGCTGAA	180
	GATTCAGACC GCATTGACCA GCAAGTCAGA TGAAGGCGAC ACCACATCAG CGACTACCTT	240
50	TOCTOCACOG AGATOTOCOC GOTTOGAÃOG GAAAGOOGGG COCCAATOOC CAGTOTATIGT	300
	TCAAGAGGC CAACAGCAGG CCGTCATGCC ATTCAATAAG CGAATGGGCA CTCGAGCGTT	360
55	GGCACATCAT GIGCIGGATA GCATCATATA CIACACAGAC AAGGIGGIGG TGAAGGGGCT	420

	TOGARATTIC TOCOCCASCT TACCTICCAR CACCTOCICG COCACARGOC TOROCCGICG	480
5	TGTAAGGAAA CGCATTGGTC TCGAAGGCGC AAATGATGTC TTTGTATACC GCACAAAAGA	540
	CCTGGTATTC GATAGTGATG AAGATATACC CAGAACCTAA CTACTTGTGT CGATATTTCT	600
10	CACACOGOCT GGTGCGGAAC COOCGCATA CATTCGTTTT ACACAAGAGG GGTTGATGCA	660
	TAAAACGCGC TT	672
15	(2) INFORMATION FOR SEQ ID NO:968:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1596UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:968:	
	GATCTTCGTA TCCATGTCGC AAAGCTCCTC CAAAATCTTT TCGTCTCCAT CATGAGAGGC	60
40	TGCTACAGCT TTTGAGCCGA TAGAATTGGA AATACCATTG GAGATTGCTA TTAGTAGGAA	120
	GACAATATAA GTACCATCTG TOGATGGGGC AGAGGCTTTA TCAAGAAGGT CCATCAGCTT	180
45	GITCITIGGAT ACAGCAGICT CATITAATAA TAATGCCTGC TCACCACTGG GCAAAAATTC	240
	AGAAACATTG AGCAGTTCAG AGAGTGAGTT CGACTCAAAG TTTTCGGTCA TTGTCTCTAA	300
50	CAAGACAAAA ACAAGGTCCT TOCTOCTCTC ATGAACATCA TAAGCCTTGA AAACCTCGAG	360
	CAAAATAGTA TIGICCIGGA TCACGITCAA AAATACCICT AGAATTAAIG CCTTCCICCA	420
55	CAATAAAGIG TCAGATTTAG GAGACAGAGI GTGGATTAAT AATGATAAAA TAACITCCAA	480

	TICCAATICC ACCAATGICA AATACIGAAC CITTIATGAGA ATGIAATACA TCTGGCCCTA	540
5	CGAACCACAA TTOCAAAATT TTTOGATGAG GAAATGTACC TCAATAGCAG CGGCACCGCC	600
	TTTGTTCOCA ACAGAAATAA CAGATCTOOG TGTGTCAAAA ATAATAATTC ATAGTTCAAT	660
10	AAAACCAGTT CTAGGAGCTC TAATCCATAC TCCTCATTTA TGCAATTGCT ATCCAGCAAT	720
	ਰਾ	722
15	(2) INFORMATION FOR SEQ ID NO:969:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(-, 555	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1597RP	
3 0	(ii) (MARIAGE). PROLITING	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:969:	
	GATOCATCAG COCCCCTACG GAAATCCTGC CCATAGAATG ACTCTCCAAA CCCCTCTGAA	60
	CHARLES A LOCATION OF THE CONTRACT OF THE CONT	
40	CTATCAGCAA AAGCTCAACA GCATRCAGGG GTCGCATGCC CAGCAAAAAAC AGATCCAGCG	120
	MCINCONTINUOS COMPONENTES EN TENERO	
	TCAGATAAGC GCTGCCARCG CACTOGATGA CGGGAATACC ATCACCGCAA TGGTCCAGCA	180
45	TITICATIOCCC AAGAAGAAAG ACCAOCCACC GCAGCAACAG GCACCCIATIG GCTCTCCCCC	240
	AAACTCTGGC AACAGCTCCA CGTACGGCGG CAGCCCTGCT GCCACGGCGC CGTCTGCATC	300
50	CGTAAATGCT CCCCCCCCCC ATCACGCCCA AAACGCTGTG CCACAGCCGC ACAGCCCCC	360
50		
	TECECTATICE GCTAACEGTA ACACAGCCCC TATGTCGCCA AACTOGGTTA GCCTTAGTAA	420
65	TOGCTCATCA GCAGGGCCCG GTTTGTCACA ACAGTCAAAC TCTCTGGACT GGAAGCAGAC	480
55		-100

	ACCOCCANAC AGROCOGAA GCGTAACCAA AACAAACCA AACCICOCTC TATICOCTAA	540
5	GAAAAAATAA TATCATGCGA CCTATCATTT ACACATATTC TAACGTTCCA CCTGTGTTAG	600
	TGTACTCATT TAATTAATTC ATTAGTGCTG CCACTGCTGC AGACATGTGG CAAGAGGCAA	660
10	AAATGGTTCC TAGCGGCATC GAACCGCT	688
	(2) INFORMATION FOR SEQ ID NO:970:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
	(B) TYPE: mucleic acid	
20	(C) STRANDFINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genamic)	
25	(-i) obtains agreem	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1597UP	
	(A) Chomiton: Prototorio	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:970:	
35	GATOGAGGCA GCCGTACCGT CTTTTGGTAC GCATGCGCAG AGTACTGCCG GATACAGCGC	60
	AACATCITAC GCTGACTACA GTTCCTGGAC ACACCACCTT ACAGCTTTGG GCCTGCGTTA	120
40	TTGGTGCTCG AAGATATGAT GTTCGGAAATT TTTCACTCGC CGTCCGGCCT GATGAAACTG	180
	GAAGACAAGA CCTACAGTCA TCTAGCCAAC ATAACGCCCT GTAGTCGGGC TCTCGAACCG	240
45	AGCETAGAGE GTAGGAGATG CTCCACGCGC CCCCGGTGCGT ACAGAGAAGA ACAAGACGC	300
	COOCATTCTT TTTATTTACT TGATTAAACT CTTGGCCAGT CTGGTTTCCA CTGACAAAGT	360
50	OCCCACCACA TOGATICOCOG GODGOGFIGAT CCTIOCCCCGG CGATIAGCGGG CGACCGGCAC	420
	TTGCGTGGGT TTCACCTGCA TCTGCACAAG ATGTTGCTAC GGGGTAGAAG CAGGGGTGG	480
55	CASCOCACO GOCOCCAAAC AGGACGTICAG TCTGACGCGC TACTTGGCCC GCGCTGCTGC	540

	ACCIDENTAL FIGURACION GRANDICO GATTOCIANO TIGAGICANA GIOTCADINA	600
5	TTATCSCATG GIGTTACTOG CGTTGCACGT GACCACACTG TGGCGTCCTT TTGGCCCACA	660
	GATGAACCTG CCATCAGCTC TCCGCCAGGA CGGTCACAAC AGGCAGGAGT AC	712
10	(2) INFORMATION FOR SEQ ID NO:971:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 740 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1598RP	
25	(A) OMBRIGHT FASTUSORF	
30	(xi) SPQUENCE DESCRIPTION: SPQ ID NO:971:	
30	GATCCTCATA ATCATAGTAC AATATCATTT CCAATAAATG GAATAGCACT AAATAAATTA	60
	GIAATAACAG TAGCACCICA AIGIGACAIT IGICCATATA CIAAACAATA ACCTAAGAAA	120
35		
	OCTOCTOCTA TAGTTAAAAT AAAGATAATA ACACCAACTG TTCATACAAT AACTCTAGGI	180
		0.10
40	GATTIATAAG AACCATAATA TAAACCTTTA CCAATATGAA TATACATACA AATAAAGAAG	240
	AATGAACCAC CATTAAGATG CATATATCTA ATTAATCAAC CTAGTTGTAC ATCTCTCATA	300
	marale difficult difficult functions.	500
	ATATOTTOTA CTGATGAGAA AGCTAATTCA ATATTAGATG AATAATGCAT AGCTAAAAA	360
45		
	ATACCAGIAA GAATTIGAAT AACTAAACAT AAACCIAATA AACAACCTAA ATTTCATCAA	420
50	TAATTAATTG ATGATGGTTG AGGTGAATCA ATAACATAAC	480
	AAATTIGATT TICTATATGC CATATATITT ATTATTAAAA TATTATTAAA TIATTATTA	540
	THE PROPERTY OF THE PROPERTY O	240
55	ATAAATATTA GATTATAATA TAATTCTITA TAATAAATTA TAATATTTAA TTAATATATT	600

	AATTIATTAT TTATTATTIA TIAATATTIA TATAATCTIT ATAGGGAATT GAACCIAATA	660
5	AACCATTAAG ATTTAATTAT TTAATTATTT AATTTATTTA ATTATT	720
	TTAAITAGAG AGATAAGGGT	740
10	(2) INFORMATION FOR SEQ ID NO: 972:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1598UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:972:	
30		
	GATCTIATOG TCTAATOGTT ACGACATCAT CTCTTCATGT TGAAAATATC GGTTCAATTC	60
	CCATTAAGAT TATTAATATA TITTAATAAT TATTATAATT AACAATATTA ATTAGAGGG	120
35		
	TACCAACATA TIGCTAACTA GCAATAGGGG TGTGTACCTT ATCTCTCTAA TTAATAATTT	180
	ATAAATTAAA TAATTAAATA AATTAAATAA TIAAATAATT AAATCTTAAT GGITTATTAG	240
40		
	GTTCAATTCC TATRAAGATT ATATAAATAT TAATAAATAA TAAATAATAA ATTAATATAT	300
45	TAATTAAATA ATATAATTA TTATAAACAA TTATATATA	360
40	TAATTTAATA ATATTITAAT AATAAAATAT ATGGCATATA GAAAATCAAA TITTATATTTA	420
		42.0
**	AATTTAGTTA ATAGTTATGT TATTGATTCA CCTCAACCAT CATCAATTAA TTATTGATGA	480
50		
	AATTTAGGTT CITTATTAGG TITATGTTTA GITATTCAAA TICTTACTGG TATTTITTTTA	540
55	OCTATOCATT ATTCATCTAA TATTGAATTA OCTTTCTCAT CAGTAGAACA TATTATGAGA	600

	uniditions insortant rational absorbers applicate artefulli	000
5	ATTIGIATG: ATATICATAT TOGGTAAA	688
	(2) INFORMATION FOR SEQ ID NO:973:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 625 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1600RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:973:	
30	GATCTAAAAG AATCCATGTA TGTACACATA TTACGGAGGG TTAAGGTGAC GAACGGTAGC	60
	TACAGGOCTA TAAATOTGGG TICCTITIGCA AAAGITICATG CAACTCATCT GGGACGITIGC	120
35	GOCAGTOTTO GOCAATOCAT TICCTTATCC TATOCTCATC GOCCTGTGCT AGTATATCTA	180
	CITCAACACA OCICCIOSCA CATGIAAAAT TOOCASCOSC ACAGAGGACA GOOCAACAIT	240
40	CTTCAGTCCC GTAACAAACT TGTTTTCATC GTATGCTCCT ACCCATCTTC TTCCGTCTGT	300
	GITCCTTACC GITGITTAAT CATACTCCCA TATAATCITC TATTAACTTC TCTCCGTATG	360
45	GGGGCAAGIT TTTGGGCCTG TAGTCGCCCA CATATTTGCA CCTCCAGTAT ACAGACCAAT	420
	GTACTICACC ATATOCCOCG ATCITCCTAT GICTACCAAG GITACCCACA TAAACGITTI	480
50	TOCATTOCA ATTITTATOT TOAATOCTTA TOCOCATGAA CATCATTTOC ACTATOCACC	540
	AGGCAATGAA CTGAAATATA CTCTTTGTTC CATGTCCATC GTTCTTTGCT GGCCGGATTA	600
55	TACATCTOCC GAACCAACCC CTCCC	625

	(2) INFORMATION FOR SEQ ID NO:974:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 656 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1600UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:974:	
25	GATCAAGCAG CTACTGCTCA CCTGCAACAA GCAGGGCCAC AAGGCCCTGC TCTTCACCCA	60
	GTOCAGGCAG ATGCTOGACA TOCTOGAGGC CTACATCTOG CACAAAGATC COGAGCTBGC	120
30	AGGCCTACAG TACCTCCGGA TGGACGGAAC CACAAACATC GCACACGGGC AGGCCCTGGT	180
	GCACCGITTC AACAACGGCC CGTACCACCT CTTTCTTCTG ACCACCGGG TGGGGGGCCT	240
35	CGGCGTCAAC CTCACGGGGG CGAACAGAAT CATCATCTTC GACCCCGACT GGAACCCCTC	300
	CACGGACCTG CAGGCCCCCG ACCOCCCCTG GCCCATAGCC CAGAAGCCCC ACGTGACTAT	360
40	CIACCIGCIC ATGGICGCCG GCTCCATCGA GGAGAAGATA TACCACCGCC AGATCTTCAA	420
	GCAGTITICTC ACCAACAAGG TCCTCAGCGA CCCCAAGCAG AAGCGCTTCT TCAAGATGAA	480
45	CCASCIGCAC CACCICITCI CCITCOSCOC 666C6CC6CC AGCGACICCI TIGCCICIGA	540
	GATGGAGCAG CAGACCOCCT CCCTCCCCCC CCAGCCCACCC CCCCACGCAC CCCCACGACCTA	600
50	CGACTCCGTC CAGCGTTTCG AGGGCGTCTC CAAGCTGCAG GGCTTCTTCA ACGCCA	656
	(2) INFORMATION FOR SEQ ID NO:975:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 715 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1601RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:975:	
20	GATCTITITC CCCCCCAAAC CGCACACCTC GTTCCAGGGG TACTTCGGCA ACAAAAAGGC	60
	CACCICAGACC AAGGITCTAC COCATGITTIT CACCAACCICA CATCCATGGT ACCCGTCACC	120
25	CGATCTCTTG AAATCCCACA AGTACCCCCA ATCCTACTTC GTCCACCCCA TGCGTCATAC	180
	GTACCGGIGG AAATCCGAAA ATGTCTCGAC TACCGACGIG GAGAATCAGT TGCTCTCGIT	240
30	CAACAAGGAC CICTITGACT GITTIGGITGT AGTGGGCCTG AAGAITTOCAA GCTACGAGGG	300
	TAGAGOOGG TTTGCTGTTA TOCAACTGAA TOCAGOOGG CGCGGACTGG ACCATGCCAG	360
35	THIGHTAGAC GACCTIGICG AGIATHIGAA ACATGCTCTT CCTCCGTAGG CCTTGCCGCT	420
	GTTCATCAAG TTCACAAACC AGCTGGAAAC AACCGATAAC TATAAGTTCG CCAAGAAACA	480
40	GTACAAAAAC CAGCAGTIGC CTCATGGTGC GGATGCGGAC GACACAATTT ACTGGTTAAA	540
	AGACTACTOC CAGTACAAAG TOTTGACOGA OGAGGACTGG GAGCAGATAT CAACOGGAAA	600
4 5	OGCANAGCIT TAGACCAGAC ANTOCCOGGA TIGACACCOG TAGGGAGITC ANANTANANA	660
	AAATACCTOG GAAGCCATCC ATAAAAGCCA TIATCAACTA TAGAAATAGA AAAGT	715
50	(2) INFORMATION FOR SEQ ID NO: 976:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
55	(B) TYPE: nucleic acid	

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1601UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:976:	
	CATCOCCCTG TCCCCCCCACCCCCCCCCCCCCCCCCCCCCCCCC	60
20	TGTGCATGAA ACTCGAATCG AACGCCGTAC TCGATGGTAG AACTAAACGG GCTCCGCTTC	120
	GAAGTACGCA CAGTTGAGTG AAATGTCAGT GTCGGCGCAAA OGCGCCCAAG ACCAGAATAG	180
25	CATGGACATC GAACAGAGGT CATCGCAGCC GAGTCGAAGC AACAGCCATG CAGGATCGCC	240
	OGGGTACGAA AAAGTGCAGC OGCTGTATGC CGCAGAGAAC GGTTCCACGG AGACTGCCCC	300
30	GACAGOCACC GOOCTIGITTIG ATAGCTCCCA CGTTGTACCG GTGTCGCAAC GOOCGCACT	360
25	CCTGAGTAGG CTGGCCCCTTG TGCCCCGAATT CCGGCAGGCA CGTCTCTATC CCCGGGGGGT	420
35	CAAAAACCTG ATCCTGGTCA TCGTCGCCTT TGCATGTATT CTGGGTCCCCA TGGGGACCAA	480
40	CATCATCTAT CCTGCCATCG GGACTATCAT GCAGGATTTT GGCACTTCGC GGTTTCTGGT	540
-10	CAGIGIGICT GTAGGCACCT ACCTOSCIGC GCTGGGCATC TICCCCATCT GGTGGTCGTC	600
4 5	OCTOSCOGAL AAAAACOGOC GOOGAACAGT GTACGTOCTG TOGTTOSCOC TOCTOGTOGT	660
	GITCAGOGIT GOOCACGGCT TCTCGCGCCAA CATCGAGAC	699
50	(2) INFORMATION FOR SEQ ID NO:977:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 704 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: INA (genamic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1602RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:977:	
15	GATOCAAGOG COCGCACAAC CAGOGATGTT TGCAACATAT TOGGCTAGTA TTCTCOCGTTC	60
	GACTITIACOC CIGOGIAGOS TIGOOGICAG ACTGCIGAGO CAGGAAACTO GGOGGGCCAT	120
20	TEAGROSCE ATTICCTOTE COCCAGTEGT TOTETTCATE AAGGOCACCC CAGAGTTCCC	180
	TCAATGTGGC TTTTTCGAAGG CCGCCATTGA GATCCTGGGC AGACAGGGGG TGGATCCTGC	240
25	GAAGTITICOG COCTTCAACC TOCTOGACCA TICTGACCTG COCACCOCCA TAAACCAATA	300
	TICCGAGIGG CCTACAATIC CACAGCICTA CGICAACAAG GAATTIGIIG GGGGGIGCCA	360
30	CATCCTCACC AACATGGGGC AATGCGGGGGA GCTAACTACT ATGCTGGAGG AGGCATGCGT	420
	TCTTGTGCCG CATACTGAGT GATGCCGCGTT ACGGCTCCCG ACTATATTTA TAGGAATACA	480
35	CCTIGEAATT TACCACTIGE ATTCTCATCC CTTTACACTT GEAAATCAIG GETGTTEAAT	540
	TCACAAACTC CGITCITTCA GITGAAAGAA GIGAGAACAG CITIOCTITICC GICATGIGIG	600
40	AAAGAGOCTT CTGATOGAGG AGGCGTGCAC ACGCCAGCAG AGAAAGTCTC TCAAAAAATG	660
	ACGITICTAGT GGAAGGGGGG ACGCAATCAC CCTTGAATGC GCGA	704
45	(2) INFORMATION FOR SEQ ID NO:978:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 476 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1602UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:978:	
10	CATOGIOCOC GOGCITGIGO TIGIOCOCAG AGITICIOCIT GIOCOCAGOC TITIOCICOC	60
15	TOCCTOOSTC GCTGCCCGGG GGGTAGTACA CGCCGAACTG CTTCAGCCGC AGCCGGCCCGC	120
	GCAAGTGCAC CGTCAGCTCC TGGTCCAGCG GAGAGACACT GCCCCAGAAC TCCAATTTTC	180
20	TOTOCTTACA CITICOAGCTO TTOTOCTICOA TOCTOCTICAC GTOCAGGTAC GTOCOGCTGT	240
	AGCCCACATT GOCATACOGG ATATTTTCTG CCTTCGAGCA GTAGTAATTC CCTCCGATGA	300
25	ANTENCANTE COCCAGCACC TECTECOCAC OGAGCAGGCC ACCTECANCE ACTETOGACA	360
	OCTICATAAT TIGIAAACOC TIGIAAAAGA ATGACTAGIA GITAGAACAG ATAAAAGAGT	420
30	OCTITIOCIGI GIOCOCTOTO OCCOGIOCAC GOCTICOGAG CICACOCOCC TICITA	476
	(2) INFORMATION FOR SEQ ID NO:979:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 724 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1603RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:979:	
	GATCOBBCAA GATCGTCGTT CAGTTGACCG GCAGATTGAA CAAGTGCBGT GTCATCTCTC	60
55		

	CANATICAN COICANACIC ANCINCOICO ACANGIOCAC TOCCANCOTA TTOCCANCON	120
5	GACAGITICGG CTACGICATC TIGACCACCT COGCOGGCAT TATOGACCAC GAGCAGGCCC	180
	ACAGAAASCA CSTTOCTOST AAGATTTTGG GTTTTGTCTA CTAAGCOOCT GCTATATAGC	240
10	GTATCTAGCT CTAATGTACG ATACTCAGTG TCTATTACGA CGGCCGCGAG CTCCACGCCC	300
	CACATACGAG COCAGOCGGC GACGOCAAGC GGGAATTCAG ATGCGTTAAT TAGCAGTAGA	360
15	TEAGRAGIAT ATATGTACAA ACAGCATACA CATGAACGOC GTOGCOGATC ATAATCTTCT	420
	ACCTOTICTA CCACCOTTOT TICTOGIAGA GICCCATGOG ATAGGAGIGA CGTOCTOGAT	480
20	ACCIOCCATT CTCAACCCCG ATCTGCCCAA ACCTCTCAAA GCACCCTGAC CACCTGCACC	540
	TOOSETCTIC CICTTOCTAC CACCOCTACC TCTCATCTIC ACCTOCACAC CACTCATCCC	600
25	GACCICCITA CACTIGGCAG CGACGICCIG AGCAGCGAAC ATGGCAGCGT ATGGAGAGCA	660
	CTOGTCTCTG TCGGCCTTGA ACTTCATACC ACCGGTAACT CTGGCAATAG TTCTCTGCCA	720
30	GACA	724
	(2) INFORMATION FOR SEQ ID NO:980:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 721 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
40	(A) ORCANISM: PAG1603UP	
	· · · · · · · · · · · · · · · · · · ·	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:980:	
	GATCTATTIG TGCCGTCCGC CATTAAGCAA GCGGCAAGCA TGGATGCAAA TCATGAGAGT	60

	ACCCIOGGC TITICACTITC CAAGOCTITA TCAACAAATC TGGTACAGGA TACATCCATC	120
5	OCCACACIAC ATATACCACA ACCOCCAAAGACO OCACAAGATO OCACTACCACT CTOCTACCTA	180
	ATCTGAGTTC GACCATATCC ACTTCGTTAA TGGTGATAGT TGATAAAAAG AAACGATACT	240
10	GAAAATTITA ATOGITACCA ATCTCATCTC ATCGCCATAC TGAAAGAATA TIGIAGGTCT	300
	COCAGTOGAA CAAGGATCAA GOOCAGOCTA AGACAATAAT GGTTOCAGOG GAGGCAGTAC	360
15	ACCAACTACC CCCACATCAA GAACAACTOC CCTTGOCTAA GCTAGTGTTT GGCCACACAG	420
	CAGACTICCA TGAAGCCTG CGAAATCCAG ACCTTAATTA TOTTTCTTCA GATGAAGACG	480
20	TATATOGOCA GGAGTOGTOC AGTGATGAOG AAGAGGGGAC TGAAATTOGT CACCTGAATG	540
	ATGACCAATT GITTITTGIG GACGACCGIG CAGATACCGA GCCAGGACCA GATGGACAAC	600
25	GEAGGCCATG GAGGTGGACC AGGTTAGCGA GGAAAGCGAC TCCGGAGAGG AAAGCGGTTAG	660
	CAGCGCTGCA TGGTCAGATT CGGATGACGA ACACTTAAAC GTTACAATAG GGCAAACCAA	720
30	T	721
	(2) INFORMATION FOR SEQ ID NO:981:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 638 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) CRGANISM: PAG1604RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:981:	
	GATCCCTATT AGAAGACSIT ACTGGGGCTC CAACCTTGGT CAGCCACACT CTCTAGCCAC	60
55		

	GAAGACUICT GGTAAGTCTG GTTCCGTCAC TGTGCGTTTG ATCCCTGCCC CACGTGGTTC	120
5	COGTATOGIC COCTOTOCAG CTGTCAAGAA COTTOCTAGAG CTTGCTGGTG TOGAGGATGT	180
	GUACACTUCC TOCACOGGUT CUACCOGUAC COUAGAGAAC ACCTUGAAGG CUGOCUTOGU	240
10	TOCCATTOST AACACCTACG GTTTCTTGAC CCCAGACTTG TOCCAGAGA ACCAGTTGCC	300
	ASCITICICCI CIAGACGICI ACGCCGACGA GGCCGTTGCC CAGAAGAAGA GAITCIAAGI	360
15	AGIGIGIGIA CATACCAACA GITTGITTICT TTGCACGIGA ACCCCCCCC TAAGCCTTTA	420
	GOCGCATGGC ACACAGACTG COGTTGGGCA GGAGATCGGT TGTCTTCCGA CGCTGGTACA	480
20	GEOCTICOCAT GOCCOTOCOCCT GCATATOCCA CATATOCCC CGTICCCCCTA	540
	CGGCAAAGAA TCAGCAAGAC ACTAGCGTCT GGCATTCTTT TTCAATGCAT TATTTAGCTT	600
25	TTTTTTTTT TTTTTTTTTA GTATAGACAC ATATAAGT	638
	(2) INFORMATION FOR SEQ ID NO:982:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: mucleic acid	
•	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: ENA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1604UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:982:	
50	GATCAGAGCA TOCCATGAGG TGGCACCGGC CGCGTCCGCT GTGTCTTTCT TCGCGGTATC	60
	GOCTICCICAA ATACTTAGCT TCTCAATACT TGGGACTGCC TTATCTTCAG AGGAAGCCGT	120
5 5	ACCATOCTOA CTOTTAGGAG COCCOTOTOC GOTGCTCTTA GOCTOCTOCT TTGTTGCCTC	180

	CICCOCCITA GCCICITCIT ICHICGCGAC AGGITICITA GCACCAACTA GCTTGATACC	240
5	CCACCIOCAA CCCAACIICA GOGICIICIT TOGITITIGCA GCAGICOCAT TOGOCACAGI	300
	TCCCTTCTCA AAGITGTTCA GCGTCACCGG AGCGGTGGCT GACTGGCCCT GTCCGTAACC	360
10	ATACCTCIGE TICCCCTTAC GGITCCCCTG TESCTIGTEAG TIGTACTCCT TGTACCTCTG	420
	ATACCCACCT TOCOCATTOT ATTOCTOGTA ACCTTOGTAG CCACCTTGTG CTGGGTTGTA	480
15	CTGCTGGTAT COCTGATAAC CCTGGTACOC GCCGGCTTGC TGGTTGTATT GCGCATAGOC	540
	TTGGTACCCA CCTGCCTGTT GGCCATACGC CTGGTAACCT CCCTGAGGCA CATACCCCTG	600
20	GRANTICTOG AAGPTACTTG GGPTGTAGTA TPOGCCGAAA TPTGCTGCCC CTGACCTTGA	660
	TITICACCIT CATOCTICOC TICCCACIGO CCTICOCICOT TOCCTICOCA	710
25	(2) INFORMATION FOR SEQ ID NO:983:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLFCULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAG1605RP	
40	(A) Charlen: Projector	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:983:	
	GATCHTCTCA AAAGTAGCAT TTACAATCTG CGTTAGCGTT GCTTGTGCAA TTCCCTGGTT	60
50	CCACCACCTT ACTGACACGA TGAAAATATT ATAGATTTGT CTGACGGCCT TTAATAGTGA	120
	TOCACCOTICA CAATTICCAAT AAGOCTICATC TIGTICAATATIA CAGCTTIGOGA GOOCGCOGAC	180
55	TACCIGCAAC TOGACCITOC CATCAGTOGC TICTCCATCA AAACAGTOGG TIATGGTATC	240

	AACGOCAGCA TCTATCAGCC GCATTCTTGG AGGTGGTGTA ACACCAGAGT CTGGCAACGT	300
5	CETECCCIEG TOSTTIGATE CIGOGGAATT TOGAGGGITG ACTAAAACAT TOTOGTOTAA	360
	COCCTTANAG GCANACANCT TIGATAGACA ATCANGAGOG CTANCCTGIN TITICTOGANC	420
10	ATTAGTTCTA CAGCAAGCAC GTAGTGCCTC AAAGACCAAC AGAGAATCCA AAAACTTTGG	480
	ATCGPTTTCA GATTGCAGGA GPTGCTCGGT CAAGTTTTTC ACAGTTTTCT CAACCAGTTT	540
15	TICATTATTA GGATGITTGT GCATGGATTT TGCTTGIAGT ATACCCTCTA ACCTTAGTTT	600
	CACAACATOC ACTGOOGATT TOATOGTOCA TGGACTACCA GAGACATTGG AATATGCCCT	660
20	TGTGTGAGATTAT GCTGGGAC	6 88
	(2) INFORMATION FOR SEQ ID NO:984:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 725 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) CREANISM: PAG1605UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:984;	
	CATCACACCA TOCCATCAGG TOCCACCOGC COCCTCCCCCT GTGTCTTTCT TOCCGGTATC	60
45	GOCTTCCGAA ATACTTAGCT TCTCAATACT TGGGACTGCC TTATCTTCAG AGGAAGCGGT	120
	ASCATOCICA CICITACCAG OSCCCTOTOC GOTOCICTIVA GOCTOCICOT TIGITOSCTC	180
50	CTCCCCCTTA CCCTCTTCTT TCTTCCCCAC AGGTTTCTTA GCACCAACTA GCTTCATACC	240
	GCACCIOGAA GCCAACTICA GGGICTICIT TOGTTTTOGA GCAGICOCAT TCGGCACAGT	300
55		

	TCCCTTCTCA AAGTTGTTCA GOGTCACCGG AGCGGTGGCT GACTGGCCCT GTCCGTAACC	360
5	ATACCTORG TICCCCTTAC COTTCCCCTG TECCTORGE TICTACTOCT TOTACCTORG	420
	ATACCCACCT TOCOCATTOT ATTOCTOGTA ACCTTOGTAG CCACCTTGTG CTOCGTTGTA	480
10	CIGCIGGIAT COCIGATAAC OCTGGIACCC GCCGGCIIGC TGGIIGTAIT GCGCATAGCC	540
	TIGGIACCCA CCIGOCIGIT GGCCATACGC CIGGIAACCI CCCIGAGGCA CATACCCCIG	600
15	GIAATICIGG AAGTIACTIG GGFRGRAGIA TIGGCCCAAA TITTGCTGCC CCTCACCTTG	660
	ATTTICACCT TCATCCTTGG CTTGCCCACTG GCCTTGGTCG TTGCCTTGCG ATTCAATTTG	720
20	ATCTT	725
	(2) INFORMATION FOR SEQ ID NO:985:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 678 base pairs (B) TYPE: nucleic acid	
30	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1606RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:985:	
	CATCAACCAT ATCAAATTTC COOCAATCTG COCCGTCATT TTTTTGCACA ACAGOCGTCT	60
45	CCACAGOGTC CATCUCCATC AGCOGAGCTA TACGTTGCGA CAGTGGCCCTC AGCTTGGTAC	120
	TOTOCCAGAG AATTGAGAOG CCCTTOGAGC TOGCTGTATG GTAACTGTOG TCCGTCGCGT	180
50	AGGTGGTCAA AGACAGOCAC TCTGAATACT CGCATTTCGC ATCCCGGTTG CGCCGTACGT	240
	ATCCGTCGCC COTTOGACTTG ATCCCCAGGC TGTCCCGAGCA CGAAGACAGC GAAGGTAGTC	300
cc		

	TOURISECTO CONCOCCAN ACCITCUIACH CLARCACALA CICGRIGIGI CCCCICCOCC	360
5	TCATEFICIT COCCICAGIT COCCACAACG CICCCGACCA TCCCICCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	420
	TICIGIOGAA OCOCCCAAAC ATTAAATICTA OCTOCTTCTT CCTOGTACTC TGTTCCCTCT	480
10	GITTCTGCCC GGCGAGCCCC TCGGATTCAA TCTCTGTACA GCCTTTATGC CGCACTTGCT	540
	CGTCCTAATT GOCTGCCACA CTCCTGCTGC TCGAACCTAA GOCGTCTGTA CCGAACCCTT	600
15	TOGPICACIT CACOGUIGOS GOGIAATOTA TEATTOCAAC CUTGIAAAAG COCCUTTCIG	660
	TACGCTATTA GITTAGCCC	678
20	(2) INFORMATION FOR SEQ ID NO: 986:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 703 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1606UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:986:	
	GATCOGCTTG AGTACTGAGA TATTAAGTCA ATACCAGGAT AAGCTTTCAA AGCACOGTAA	60
45	TOCTACIGIG CAATOGTOOG GACCTACTGA TITICTOCCAC TACGTCCTAG COCCTGAAAT	120
	TTIATCATAC GIGTOCCCAG ACCAACTOGG CCTTOCAGAT ATOGATGAGG CTTOCACTTA	180
50	CATGGAAAGT ACCACGGAAT ACGGGTTAAA TGTGGCGGAC GAAGAGCCTC TAGATATTTG	240
	OCAATTAGAA TACGAAGAGA AAAAGCTOCA ACOGTTAGGA TTAGGACCCA AGTACAGCAG	300
55	CATGACTIAC AGAAAGCATC CIGCCAGGGC GTCGGCTGTA TTAGATACAT CCAAAAAATGG	360

ATCHTACANT COTACTANCT ANTACATACC COCCTTATES ANTICOCTIC TOCACGEAN GITGCATATE CEARANCAIG CTRIDOCRIE GATGATOCC TACCACTITIT TANICOGNI ARACIGGACT ACCCATANAT ACTACTITICA ATROCGATAT ATA (2) INFORMATION FOR SEQ ID NO:987: (3) SEQUENCE CHARACTERISTICS: (4) LENGTH: 622 base pairs (B) TYPE: mucleic acid (C) STRANDENESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PRO1607RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: CATCACACGA CAGTOCOAGT COGGGCAGGA GACGGAAGAC CTGTUGAGGG TCATGGGCAC COTTGGCTCC GACCTGCACC GIGTUGCCAT TOTGGACTIC ACCTCTACT CTATCCOTG CATTCTGTGG CACCGACGTC TGATGAAGTA CCTGTGGGAC ACCTCTTCACCACTACACTA	TTCTAAAGAG CATAAGCGTA AAGGAAAGCA ACACAAATTA AAAAAAGGAC AGCAGTCTAC	420
GITGCATATG CGAAAACATG CTATGCAGTG GATGATCGCG TACCACTITT TAATCOGAN AAAGIGGACT AGCGATAAAT AGTAATTICA ATAGCGAATG TGAATTIGAA TTGAGAATT GCAATAATGCT GIGGATTTCT GTGATTATAA TACCATAAAT ATA (2) INFORMATION FOR SEQ ID NO:987: (i) SEQUENCE CHARACTERISTICS: (A) LENSTH: 622 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOROLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) GRIGINAL SOURCE: (A) CRCANISM: PRG1607RP (A) CRCANISM: PRG1607RP CATCACAGA CAGTGCCAGT CGGGCCAGC GGTACCGGTT GCCCCAGTG TGAACCTGAA CCTTGGACTAC CGCTCCACA CAGTGCCCAA GAGGGAAGAC CTGTCGACGG TCATGGGCACA CCTTGGCTCC GGCGGCACC GTGTCCCCAA CACTGTCCAC ACCTCTCAT CTATGCCGGC CATTCTGTCG CAGGGACGTC TGATGCAAGTA CCTGTGGCAC AACCCCCCC AGTTCACCAC CCTGGCAGGTC CTCCTCAACT CGTCCCTCCA AAAGTTCCCCA ACCCCCCCC AGTTCACCAC CCTGGCAGGTC CTCCTCAACT CGTCCCTCCA AAAGTTCCCACACAG ACCCCCCCCC CCTGCCCCCT ACTTCCCCGCC AGTCCCCCCC ACTTCCACCACAG ACCCCCCCCC CCGTTCCCCCTC CACAAGATGC ATACACACAG GATGTTCCCCC ACCCCTCCCCCCCCCC	AAAGATAAGG GTATCAAAAA AAAGOOGAGG OGTACAACCA CACAGCATAT GOGATTAATA	480
AAAGIGGACT ACCGATAAAT ACTAATTICA ATACCGANIG TGAATTICAA TICACAATT GGATAATCCT GIGGATTCT GIGATTATAA TACCATAAAT ATA (2) INFORMATION FOR SEQ ID NO:987: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 622 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SCURCE: (A) ORGANISM: PAGI607RP (AI) SEQUENCE DESCRIPTION: SEQ ID NO:987: CATCACACGA CAGIGCOAGT COGGCCACC GGTACCGGT GCCCCCATCG TGAACCTCAA TCCGAAGAAC CCCTTCTACA AAGICCCCCA GACGGAAGAC CIGICGACGG TACTGCGGG CCTTGGCTCC GCCCTCCACC GTGTCGCCAT TGTGGACTCC ACCTCTTCAT CTATCCGGGG CATTCTGTCG CACCGACGT TGATGAAGTA CCTGTGGCAC AACGCCCCC AGTTCACCAA CCTGGAGGTG CTCCTCAACT CGTCCCTCCA AAAGITCCCCA AACGCCCCCC AGTTCACCAA CCTGGAGGTG CTCCTCAACT CGTCCCTCCA AAAGITCCCCA AACGCCCCCC AGTTCACCAA CCTGGAGGTG CTCCTCAACT CGTCCCTCCA AAAGITCCCCA ACCCCCTCCCC TACCCCTCCT ACTTCCCCCCC AGTCCCCAACG GATATCCACTC ACCCCCTCCCC CCGGAGGTG CTCCTCAACT CGTCCCCTCCA AAAGITCCCCC ACCCCTCCCCC CCGGACGTG CTCCTCCAACT CGTCCCCTCCA AAAGITCCCATC TCCAACCACG ACCCCCCTCCCCCCCCCCCCC	ATCTTACAAT CGTACTAAGT AATACATACC GOGCTTATAG AATCTGCTGC TGCACGGAAA	540
15 GGATAMIGUT GIGGATITUT GIGATIATAA TACCHTAAAT ATA (2) INFORMATION FOR SEQ ID ND:987: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 622 base pairs (B) TYPE: Incleic acid (C) STRANDEINESS: single 25 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI607RP (A) ORGANISM: PAGI607RP (A) ORGANISM: PAGI607RP CATCACACGA CAGTGCCAGT COGGGCAGGC GGTACCGGT GGCCCATCG TGAMCCTCA TCCCAAGAAC CCCTTCTACA AAGTCCCCCA GACGGAAGAC CTGTCGACGG TCATCGGCA CCTTGGCTCC GGCCTCCACC GTGTCGCCAT TGTGGACCAC ACCTCTCAT CTATCCACA CCTTGGAGGTG CTGCTCCACT GGTCGCCTAC ACCTCTCAT CTGTCGACCAC CCTTGGAGGTG CTGCTCCACT GGTCGCCTACA AAAGTTCCACC ACCTCTCACACAG ACCCCCCCC TACCCCTCCT ACTTCGCCGC AGTCCCCTCT TATTTCCACTT CTCGACACAG ACCCCCCTCC CGTTCCCCTC ACCTTCCCCCC ATACACACAG GATATTCCACT ATTCCACACAG ACCCCCCTCCC CGTTCCCCTC ACCTTCCCCCCC ATACACACAG GATATTCCACTC ATTCCACACAG ACCCCCCTCCC CGTTCCCCTC ACCTTCCCCCCC ATACACACAG GATATTCCACTC ATTCCACACAG ACCCCCCTCCC CGTTCCCCTC ACCTTCCCCCCC ATACACACAG GATATTCCACTC ATTCCACACAG ACCCCCCTCCCCCCCCCC	GITGCATATG CGAAAACATG CTATOCAGTG GATGATCGCG TACCACTTTT TAATCCGATA	600
(2) INFORMATION FOR SEQ ID NO:987: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 622 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI607RP (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACAGGA CAGTOCCAGT COGGGCAGGC CGTACCGGTT GOCCCATGG TCAACCTCAA TOCGGAAGAAC CCCTTCTACA AAGTCCCCGA GAGGGAAGAC CTGTGGAGGG TCATGGGCAC CCTTGGCTCC GCCTCCACC GTGTGGCCCAT TGTGGACTCC ACCTCTTCAT CTATGCGGGG CATTCTGTCG CACCGACGTC TGATGAAGTA CCTGTGGGAC AACCCCCCC AGTTCACCAC CCTTGGAGGTG CTGCTCAACT CGTGGCTGCA AAAGTTGGGC ATCGGTGGCACCAC CCTTGGAGGTG CTGCTCAACT CGTGGCGTGT TATTTTCCATT CTGCACACAG ACCCCCCCCC TACCCCTCCT ACTTGGCGGC AGTCGCGTGT TATTTTCCATT CTGCACACAG ACCCCCCCCC CGTTGCCCCTG CACCAAGATGC ATACCACAGG GATGTTCCTCC ATTCGCACTGCCCCCCCCCC	AAAGICGACT AGCGATAAAT AGTAATTICA ATAGGGAATG TGAATTIGAA TTGAGAATIG	660
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 622 base pairs (B) TYPE: mxcleic acid (C) STRANDENESS: single (D) TOROLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SCURCE: (A) ORGANISM: PAGL607RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACCA CAGTOCCAGT COGGGCACCA CAGTOCCATCA TORACCTOM TOCCAMARA COCCITICIACA ANGIOCCOCA GAGGGAAGAC CIGIOGAGGA TORTOGGCA CCTTOGCTCC GGCGTGCACC GIGIOGCCAT TOTOCACICC ACCITICAT CIATOCGGG CATICITICS CAGCGACGTC TGATGAAGTA CCTGTGGGAC AACGCCCCC AGTTCACCAC CCTGGAGGTG CTGCTCAACT CGTGCCTCCA AAAGTTGCCC ATCCGTGGCACC TACCCCTCCT ACTTCGCCCC AGTCCCCTCT TATTTCCATT CTGGACACAG ACCCGCTGCC CCGTGCCCCT ACTTCGCCCC AGTCCCCTCT TATTTCCATT CTGGACACAG ACCCGCTGCC CCGTGCCCCTC ACTTCGCCCCC AGTCCCCTCT TATTTCCATT CTGGACACAG ACCCGCTGCC CCGTGCCCCTC CACAAGATGC ATACAGAACG CATATTCCTCC ATCCGCTCCC	GCATAATGCT GIGGATTTCT GTGATTATAA TACCATAAAT ATA	703
(A) LENGTH: 622 base pairs (B) TYPE: mxcleic acid (C) STRANDEINESS: single 25 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGL607RP 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACCA CAGTOCCAGT COGGGCACCC GGTACCCGTT GCCCCCATCG TCAAGCTCAA TCCCAACAAC CCCTTCTACA AAGTCCCCCA GACGGACGAC CTGTCGACGG TCATGGGCAC CCTTGGCTCC GCCGTGCACC GTGTCGCCAT TGTGCACTCC ACCTCTTCAT CTATGCGTG CATTCTGTCG CACCGACGTC TCATCAAGIA CCTGTGGGAC AACCCCCCCC AGTTCACCAC CCTGGAGGTG CTGCTCAACT CGTCCCTCCA AAAGTTGGCC ATCCGTGGCACC TACCCCTCCT ACTTCGCGGC AGTCGCGTGT TATTTCCATT CTCCACACAG ACCCGCTGC. CCGTTGCCCTG CACAAGATGC ATACCACAACG GATATTCCTC ATCCACACAG ACCCGCTGC.	(2) INFORMATION FOR SEQ ID NO:987:	
(B) TYPE: mxcleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGL607RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACCA CAGTOCCAGT COGGGCACCC GETACCCGIT GOCCCCATCC TCAAGCTCAA TCCCAACAAC CCCTTCTACA AAGTCCCCCA GACGGACGA CTGTCGACGG TCATGGGCAC CCTTGGCTCC GCCGTGCACC GIGTGGCCAT TGTGGACTCC ACCTCTTCAT CTATGGGGCA CCTTGGCTCC GCCGTGCACC GIGTGGCCAT TGTGGACTCC ACCTCTTCAT CTATGGGGCA CCTGGGGGGG CTGCTCAACT CGTCGCTGCA AAAGTTGGGC ACCTGTGCACC TACCCCTCCT ACTTCGCGGC AGTCGCGTGT TATTTCCATT CTCCACACAG ACCCGCTGC CCGTTGCCCTG CACAAGATGC ATACGGGGG GATATTCTTC ATTGGACACAG ACCCGCTGC	(i) SEQUENCE CHARACTERISTICS:	
(C) STRANDELNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGL607RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987: GATCACACGA CAGTGCCAGT COGGGCAGCC GGTACCCGTT GGCCCATCG TGAAGCTGA TCCGAAGAAC CCCTTCTACA AAGTCCCCGA GACGGAAGAC CTGTCGACGG TCATGGGCAC CCTTGGCTCC GGCGTGCACC GTGTCGCCAT TGTGGACCCC ACCTCTTCAT CTATGCGCAC CATTCTGTCG CAGCGACGTC TGATGAAGTA CCTGTGGGCAC AACGCCCGCA CCTGGGAGGTG CTGCTCAACT CGTCCCTGCA AAAGTTGGGC ATCCGTGTGC TACCCCTCCT ACTTGGCGGC AGTCGGGTGT TATTTCCATT CTGGACACAG ACCGCCTGCC CCGTGCCCTG CACAAGATGC ATACGGAGG GATATCCTCC ATCCGACACAG ACCGCCTGCC CCGTGCCCTG CACAAGATGC ATACGGAGG GATATCCTCC ATTGCACACAG ACCGCCTGCC	(A) LENGTH: 622 base pairs	
(ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGL607RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987: GATCACACGA CAGIGGGAGT COGGGGAACGA CAGIGGAACGA TGAAGCTGA TCCGAAGAAC CCCTTCTACA AAGIGGGGA GAGGGAACGA CTGTGGACGG TCATGGGCA CCTTGGCTGC GGCGTGCACC GTGTGGCCAT TGTGGACCTC ACCTCTTCAT CTATGGGCA CATTCTGTGG CAGCGGAGT TGATGAAGTA CCTGTGGGAC AACGGCGGC AGTTCAGCA CCTGGGAGGTG CTGCTCAACT CGTGGCTGCA AAAGTTGGGC ATGGGTGC TGCATGCCAC TACCCCTCCT ACTTGGGGGC AGTGGGGGGT TATTTGCATT CTGGACACAG ACCGCTGCC CCGTGGCCCTG CACAGGATGC ATACGGGGT TATTTGCATT CTGGACACAG ACCGCTGCC CCGTGCCCTG CACAGGATGC ATACGGACG GATATTCCTC ATTGCACACG ACCGCTGCC	(B) TYPE: nucleic acid	
(ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGL607RP (xi) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACCA CAGIGCCAGT COCCCCAGA GACGCAAGAC CIGIOGACGA TCAAGCTGAA TCCGAAGAAC CCCTTCTACA AAGICCCCCA GACGCAAGAC CIGIOGACGA TCATGCCCCA CCTTGGCTCC GCCGTGCACC GIGICGCCAT TGTGCACTCC ACCTCTTCAT CTATGCCGTG CATICTGTCG CACCGACGTC TCATCAAGTA CCTGTGGCAC AACGCCCCCC AGTTCAGCACAC CCTGGAGGTG CTGCTCAACT CGTCGCTGCA AAAGTTGCCC ATCGGTGTCC TCGATCACCAC TACCCCTCCT ACTTCGCGGC AGTCGCGGTG TATTTCCATT CTGGACACAG ACCGCCTGCC CCGTGCCCCTC ACTTCGCCGCC AGTCGCGGTG TATTTCCATT CTGGACACAG ACCGCCTGCC CCGTGCCCCTC CACCACAGATGC ATACCACAAGG GATATTCCTC ATTCCACCACAG ACCGCCTGCC	(C) STRANDELNESS: single	
(vi) CRIGINAL SOURCE: (A) ORGANISM: PAGL607RP (A) ORGANISM: PAGL607RP (A) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACGA CASTGCCAGT COGGGCAGC GGTACCGGT GGCCCCATCG TCAMCCTGA TCCGAAGAAC CCCTTCTACA AAGTCCCCGA GACGGAAGAC CTGTCGACGG TCATGGGCAC CCTTGGCTCC GGCGTGCACC GTGTCGCCACT TGTGGACTCC ACCTCTTCAT CTATCCGTG CATTCTGTCG CAGCGACGTC TGATCAAGTA CCTGTGGGAC AACGCCCGC AGTTCACCAC CCTGGCAGGTG CTGCTCAACT CGTGGCTGCA AAAGTTGGGC ATCCGTGTGC TGGATCCACC TACCCCTCCT ACTTCGGGGC AGTCGGGTGT TATTTCCATT CTGGACACAG ACCGCCTGCC CCGTGCCCCTG CACAGGATGC ATACCAGAACG GATGATCCTCC ATCCGACACAG ACCGCCTGCC CCGTGCCCCTG CACAGGATGC ATACCAGAACG GATGATCCTCC ATTCCACACAG ACCGCCTGCC	(D) TOPOLOGY: linear	
(A) ORGANISM: PAGL607RP (A) ORGANISM: PAGL607RP (AC) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACGA CAGTGCCAGT CCCCCCAGC GGTACCCGTT GCCCCCATCG TGAACCTGA TCCGAAGAAC CCCTTCTACA AAGTCCCCCA GACCCAAGAC CTGTCGACGG TCATGCCCAC CCTTGCCTCC GCCGTGCACC GTGTCGCCAT TGTGCACTCC ACCTCTTCAT CTATCCGTG CATTCTGTCG CAGCGACGTC TGATGAAGTA CCTGTGCGAC AACGCCCCCC AGTTCAGCAC CCTGGCAGGTG CTGCTCAACT CGTCCCTGCA AAAGTTGCGC ATCCGTGTGC TGGATCCACC TACCCCTCCT ACTTCCCCGC AGTCCCCTGT TATTTCCATT CTCCACACAG ACCCCCTGCC CCGTTCCCCTG CACAAGATGC ATACCAGAACG GATATCCTGC ATCCGCTGCACCCCCCCCCC	(ii) MOLECULE TYPE: DNA (genomic)	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 987: GATCACACGA CAGTOCCAGT COGGGCAGCC GGTACCCGTT GGCCCCATCG TGAAGCTGAA TCCGAAGAAC CCCTTCTACA AAGTCCCCCGA GACGGAAGAC CTGTCGACGG TCATGGGCACA CCTTGGCTCC GGCGTGCACC GTGTCGGCCACT TGTGGGACTCC ACCTCTTCAT CTATCCGTGC CATTCTGTCG CAGCGACGTC TGATCAAGTA CCTGTGGGAC AACGCCCGCC AGTTCAGCAA CCTGGCAGGTG CTGCTCAACT CGTCGCTGCA AAAGTTGGGC ATCGGTGTGC TGGATCCACC TACCCCTCCT ACTTCGCCGC AGTCGCCTGT TATTTCCATT CTCGACACAG AGCCCGCTGCC CGTTGCCCTG CACAAGATGC ATACAGAAGG GATATCCTCC ATCGCAGAGG TGCACCACCC	(vi) ORIGINAL SOURCE:	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACACGA CAGTGCCAGT COGGGCAGCC GGTACCOGTT GGCCCCATCG TGAAGCTGA TCCGAAGAAC CCCTTCTACA AAGTCCCCCA GACGGAAGAC CTGTGGACGG TCATGGGCAC CCTTGGCTCC GGCGTGCACC GTGTCGCCAT TGTGGACTCC ACCTCTTCAT CTATCCGTG CATTCTGTGG CAGCGACGTC TGATGAAGTA CCTGTGGGAC AACGCCCGCC AGTTCAGCAC CCTGGAGGTG CTGCTCAACT CGTGGCTGCA AAAGTTGGGC ATCCGTGTGC TGGATGCACC TACCCCTCCT ACTTCGGGGC AGTCGCGTGT TATTTCCATT CTGGACACAG AGCCGCTGCT CGTTGCCCTG CACAAGATGC ATACAGAAGG GATTATCCTCC ATCCGACACAG ACCCGCTGCT	(A) ORGANISM: PAG1607RP	
GATCACACGA CAGTGCCAGT COGGGCAGCC GGTACCOGTT GGCCCCATCG TGAAGCTGA TCCGAAGAAC CCCTTCTACA AAGTCCCCGA GACGGAAGAC CTGTCGACGG TCATGGGCAC CCTTGGCTCC GGCGTGCACC GTGTCGCCAT TGTGGACTCC ACCTCTTCAT CTATCCGTG CATTCTGTCG CAGCGACGTC TGATGAAGTA CCTGTGGGAC AACGCCCGCC AGTTCAGCAC CCTGGGAGGTG CTGCTCAACT CGTCGCTGCA AAAGTTGGGC ATCGGTGTGC TGGATCCACC TACCCCTCCT ACTTCGCGGC AGTCGCGTGT TATTTCCATT CTCGACACAG AGCCCCTGCC CGTTGCCCTG CACAAGATGC ATACAGAACG GATATCCTGC ATCGGTGTA TGGACGACAG		
TCCGAAGAAC CCCTTCTACA AAGICCCCCA GACGGAAGAC CTGTCGACGG TCATGGGCAC CCTTGGCTCC GGCGTGCACC GTGTCGCCAT TGTGGACTCC ACCTCTTCAT CTATCCGTG CATTCTGTCG CAGCGACGTC TGATGAAGTA CCTGTGGGAC AACGCCCGCC AGTTCAGCAC CCTGGAGGTG CTGCTCAACT CGTCGCTGCA AAAGITTGGGC ATCGGTGTGC TGGATCCACC TACCCCTCCT ACTTCGCGGC AGTCGGGTGT TATTTCCATT CTGGACACAG AGCCCCTGCC CGTTGCCCTG CACAAGATGC ATACAGAACG GATATCCTGC ATCGCAGTGA TGCACCACAC	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:987:	
CCTTGGCTCC GCCGTGCACC GTGTCGCCAT TGTGCACTCC ACCTCTTCAT CTATCCGTGC CATTCTGTCG CACCGACGTC TCATCAAGTA CCTGTGGCAC AACGCCCGCC AGTTCAGCA CCTGGAGGTG CTGCTCAACT CGTGGCTGCA AAAGTTGGGC ATCGGTGTGC TGGATCCACC TACCCCTCCT ACTTGGCGGC AGTCGCGTGT TATTTGCATT CTCGACACAG AGCCGCTGCC CGTTGCCCTG CACAAGATGC ATACAGAACG GATATCCTGC ATCGCAGTGA TGCACCACGC	GATCACACGA CAGTGCCAGT CGGGGCAGCC GGTACCCGTT GGCCCCATCG TGAAGCTCAC	60
CATICITATOS CASOGRACITO TGATICAAGIA COTIGIGOGAC AACGOOOGOC AGITICAGCA. COTIGGAGGIG CTGCTICAACT CGTCGCTGCA AAAGITIGOGC ATCGGTGTGC TGGATICCAC. TACCCCTCCT ACTTCGCGGC AGTCGCGTGT TATTTCCATT CTCGACACAG AGCCGCTGC. CGTTGCCCTG CACAAGATGC ATACAGAACG GATATTCTGC ATCGCAGTGA TGCACCACAG.	TCCGAAGAAC CCCTTCTACA AAGTCCCCCA GACCGAAGAC CTGTCGACGG TCATGCCCAT	120
CCTGCAGGTG CTGCTCAACT CGTCGCTGCA AAAGTTGGGC ATCGGTGTGC TGGATCCAC TACCCCTCCT ACTTCGCGGC AGTCGCGTGT TATTTCCATT CTCCACACAG AGCCGCTGC	CCTTGGCTCC GCCTGCACC GTGTCGCCAT TGTGCACTCC ACCTCTTCAT CTATCGGTGG	180
TACCCCTCCT ACTICOCOGC AGTCCCCTGT TATTTCCATT CTCCACACAG ACCCCCTCC	CATTICTICTICS CAGCIGACITIC TIGATICALAGITA COTIGTIGGICAC AACGOOGGC AGTITICAGCAA	240
CGPTCCCCTG CACAAGATGC ATACAGAACG GATATCCTTCC ATTCCACTEA TICCACCAGACG	CCIGGAGGIG CTCCICAACT CGTCCCTGCA AAAGITGCGC ATCCGTGTCC TGCATCCACA	300
CONTOCCCTG CACAAGATGC ATACAGAAGG GATATCCTCC ATCCCAGTGA TCCCACTACT	TACCCCTCCT ACTICOCOGC ACTCCCCTCT TATTICCATT CTCCACACAC ACCCCCTCT	360
55	CGITICCCCTIC CACAAGATICC ATACAGAACG GATATCCTICC ATCCCAGTIGA TCCGACCACCA	420
5		AAAGATAAGG GINTCAAAAA AAAGGCGAGG GGTACAACCA CACAGCATAT GGGATTAATA ATCITACAAT CGIACTAAGT AATACATACC GGGCTTATAG AATCICCIGC TGCACGCAAA GTTGCATATG GGAAAACAIG CIATOCACTG GATGATGGG TACCACTTIT TAATCOGATA AAAGIGGACT AGGATAAAT AGTAATTICA ATAGGGAATG TGAATTIGAA TTGACAATTG GGATAATGCT GIGCATTTCT GTCATTATAA TACCATAAAT ATA (2) INFORMATION FOR SEQ ID NO:987: (i) SEQUENCE CHARACTERLISTICS: (A) LENGTH: 622 base pairs (B) TYPE: macleic acid (C) STRANDERNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: INA (genomic) (vi) CRIGINAL SOURCE: (A) CRGANISM: PAGL60TRP (di) SEQUENCE DESCRIPTION: SEQ ID NO:987: GATCACAGGA CAGTGCGGGT GGGGGGGGGGGG TCATGGGGGGT CCTTGGGTGC GGGGGGGGCT TGATCAGGAGGC CTGTGGGGGGG TCATGGGGGGG CATTCTGTGG CAGGGAGGTC TCATCAGGTA CCTGTGGGGCC AGGTGGGGGAGGAC CCTGGGAGGTG CTGCTCAACT CGTGGGGGGA AAAGTTGGGC ATGGGTGGGC TGGGAACGAC CCTGGGAGGTG CTGCTCAACT CGTGGGGGGA AAAGTTGGGC ATGGGTGGGCACAC TACCCCTCCT ACTTGGGGGC AGTGGGGGGGT TATTTGCATTC CTGGACACAG AGGCGGCGCT TACCCCTCCT ACTTGGGGGC AGTGGGGGGT TATTTGCATTC CTGGACACAG AGGCGGCTCCT

	CACCATOCIO CICOGGAACA ICICIGIGAL AGACGICAAG CACGITACOC GCACCTOGCA	480
5	GTATCCGTTG CTGCACAACA CCTGCCGCCA TTTCATCAGC GTGATCCTCA ACAACCCCGG	540
	CCIOCACATE GOCAAGCACT CCITICCOCAT CTTCCACCTT TACCCCACCT CGTCCCTGCC	600
10	CCGCACGGIU GCGAAGCTGG TC	622
	(2) INFORMATION FOR SEQ ID NO:988:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 674 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1607UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:988:	
35	GATGOGTGCC COCACCTCCG CCCCATTICTT COCCAGCTCG TTCCCCAATGT TCCGTATCCA	60
	CITCIOCITC TICATOCCAT CCACCICOGI CCCCCCCC TOCAAACCIC CCTTGGCTGC	120
40	GOOGCCACTC GTACCTGCCT GCCGTTCTTC ATCTTCAATA ACTATCACTT GCATCCCGTT	180
	AGTACCTOCA COGTOCAGAG GOCTOTAAAC CTCCCCTCAG CCCTTCAAAA COCCCCACCA	240
45	CATACCTICI CGICCIOGAA TCATGATIGC COCTGGIAAT CITCACOCTA GCACTAATIT	300
	OGICACTAAC TOCOCTUTTE COCACTORAA TTOCTOCTOC AGATOCTORA GTCTCATGTC	360
50	GICCATTICI GCCGATGITA AAATATGGGT TICCGAAAAA GCCCIGCITG CCCTIGACIG	420
	ATGCTCGACT CACAGAGGAC TCACCAGAGC TTGAACCGCA GCCAGGAAGC ATTCCTGTCA	480
55	TACCAGAAAG GGCCCACGGC GAGAATCAGA ATGGATGTTG CATAGTGGGG CAGCAAGAGT	540

	SCTOCASCOC TOSSOCIOCOS CAASCOSCAÇA TOCAACAACT COSTOCACAS CATCACAASC	6 00
5	OCTATACCAT COCTICCCCA ACCATTICOC ACCICCOCCA CTICACCAAC TATICCCCAC	660
	CTGGCCGGTT ACAG	674
10	(2) INFORMATION FOR SEQ ID NO:989:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 733 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
0.5	(A) ORGANISM: PAG1608RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:989:	
	GATCAAAACC ATCACCAAGT TIAITCATGA AGTGTCCGAC GATTTCAAGG TCATCATAAT	60
3 5	CGACGCAATT CGTACTTTGT CGCTAAAGTT CCCAGATGAG TGGAAGAATA TTCTATCCTT	120
	TITAATIGAC ACTITICAAAA GIOCAGAGOG TOGGIATACA TICAAAAATA ATATOGIAGA	180
40	TOCGCTGTTT GACCTGATCC AACATGTACC TCAGTCAAGG GAACAGGCTC TGGAACACTT	240
	GIGICACTIT ATTGAGGACT GCCAGTICAA TGAAATCICA GICAGGATCA TITACTTATT	300
45	GGGTAAGGAG GGCCCCTCGA CAGAAAAGCC TTCGCTTTAC GTTAGACACC ATTACAACAG	360
	AGPIGICITG GAAAAITCAA TCATCAGATC TOCTOCTGIT AGCOCATTGI CCAAGPITTC	420
50	CICTOGGAAG AAAGATCCGT CGTTAGCTTA TICCATCGAA AAATTGCTAA AGGGTATCCA	480
	AACCGATGAG GATGACGAAG TGAGAGACAG GGCAACCATT CTAGTAAAGC TCCTTGAGGA	540
55	GAACAAGGAA AAGCCTGGTG TTGCCGATGA ATTTATCCAG CCAAAGCATA GTTACCATCT	600

	ACTIGOCOLIG GAAAAGIAAA TIAACGAACT ATCTCCACCA TAATGAAGAT GOCTTTGCCA	660
5	CACCATTIGA COCGICGAGO ATTOCAAAGT TACACAGAAG AGGAGOTCAA GOCTATTAAT	720
	TTGAAOCAGA AAC	733
10	(2) INFORMATION FOR SEQ ID NO:990:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 723 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: LNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1608UP	
25	(A) CLOSUISM. PASIOUGUP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:990:	
	CATCIGODCA AGGATAAAGG TGTTCATCAA GTCATTGTGA ATGACOCCOG CAGCCTGTGG	60
35	COCCTIAGIG CCATTICIGA TOGICCATIC TCTGACTICG TCCGGCCCGC AGGICAAGAA	120
	CGAGATCAGA TOCAGCITCT GICTCATGGT GGTGATGATC TTTGGGAAGG CGGACTGGAC	180
40	GOOGATOTIC TOSCACTOCT CGACAGOCTC CICGGOOCTC ATGTOCGACA GICTICICCIC	240
	CAGGCACACC GAGAAGGGTA TAATTAGATC GCCAGGGGAG TACTTGTCGA TCCACTCCTT	300
45	CATCITCAAG AGGIOCITGI TCITICITTCT AATGIAGICC COCTCCCATA GGITGATCAG	360
	GIACATGGAT GOCTIGGOGG TIMOCAGGAA CATGGAGTIG ATGACCTGCA CCTCCTTGGT	420
50	GCTCCAGGAC TOGTITIOCGA CTCTCTGACC CGACTTCAAA AGCTCGATAA TGCGCTTCAC	480
	CASCIOGGC TOCTOCTICT TETETTICAE CTOCAGGGAC TOGGCCCCC TETTOCTCAT	540
55	CTTCTCCACG GOCTCCAGGT GCTTCTCCCC GAACTCAATG TCCTTCAAAC GCAATTCCGT	600

	GITAATCATG TOCAGGICTO TGACOGGGTO GACGTOACCO TCAATGTGGA TGATCTOGGC	660
5	GTOGTOGAAG CAACGCACGA CCTGGTAGAT CGAGTCCACA GATCTGATGT GCGATAAGAA	720
	gac	723
10	(2) INFORMATION FOR SEQ ID NO:991:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 692 base pairs	
15	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1609RP	
25	(ii) Gibblion	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:991:	
	GATCAGACGG TAATGGCCGG CATGCTGCGG CAGGTGCAGC ACGTATCTAG CGTCCATCGT	60
35	CICTIGCIGI GGIGGGGGG GCGGGGAAAG GGCCIGGCIG CGGGAGAAAT ACAGIAGGA	120
	TOTOTOGOGO COGOGOACCA GOGOACCOGG GOCOGCGAAC AGCGCCGTTT GCCCCTTAAT	180
40	CCCCACAAAC CCATATAAGT AGAGCCTTAG CCCCTCCTCG AGCGACGCCA GAACACACAC	240
	AAGGACCAAT GAACACGATT ATCAACTITOC AGGAAGOCAG COOGCAGGCT CTCAGCGAGC	300
45	ACASCATCTT COCAGATGTG CTGGTGTGCA CTGCTGAAAA CGGTGCATCA GGACACCTTG	360
	TAGIGGAGTA CCCCCCCCAG TCTACAGCCG TCACCCTCCCG GAACGTTATC CCTCTCCAGC	420
50	CTACOCAGAC OGTIGOCCAAC CTGATGTTAA TCACGACOGA GCCOGGAATC GTCAGOGAGG	480
	GGCACCTATT CACGCTGGGG ATGACAGACC CAGATGCTCC CTCGCGGTCG CACCACAAGT	540
55	GETCGGAATA CTGCCACTTT CTGGAAAACGA ACATAACGCT GGGCTCGGAT GACGGGGTGT	600

	CUCALUTGET GUTAAAGGGC ACCCCGCAGG TGGAGCACAT GGGCCCTGGG CCGCCGGGCCC	660
5	COCACACOGE CICACCOSTA CETETOSTIC TT	692
	(2) INFORMATION FOR SEQ ID NO:992:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1609UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:992:	
30	GATTOGAGAAG ATTTOGAGAA GGAAAGCGTC TTGGTGCTAG CCTGGTGACC CCCTGCGGG	60
	CTGGAACTGC GCGATATACT ACATAAAATA CGTTATCCCT GGAATTTGTA GCATTAAAGG	120
35	ACTIATOGAC TATTCTGIAT ACCIGOGCIT COOGCIGOCA CCCGTAGCAA TGCCAAACTC	180
	ACTOCCACCO CTOCCTOCTO COCCAACAAT COCACTOACO COCACCOCAG COCCACOCAGIC	240
40	ACGIGCOCCC COCATIOGOG CCCACATCAC TOCCCTTGCC TCCCTTCCCC ACCCCGCCAC	300
	GUEACTICOGO GOCCOCAGO COCAGOTGAT TOTAGITIGOA TAGGAAACTA GOCTAAAATO	360
45	ACCTEACTEA ATCCCCCCC CACATCATAC CATCCCACC GACCCCCCACT ACCCCCCCCC	420
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	480
50	TOTGAGAGGG COCATOCOGG COCATOCTOC ATGCCTCCCT COCTGTTCCC GAACATGTCG	540
	AGGCACGIAC GCGGGCAGCT CAGITACCCG AAGITACCCC TICTICIGAT TAAATITIGGA	600
<i>55</i>	CTGAAACTTA AAAGCOGTCA GCAGTGGCAA ATCCACGGTG AGAATAATTA CAGGAAACAG	660

	COGTOGACCA OCTOCOGAAC TAGACGACOG GTTOGTIGTOG CACOCATAGA AGGTATGTTIC	720
5		
5	(2) INFORMATION FOR SEQ ID NO:993:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 731 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1610RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:993:	
	GATCAATTIC CITTOGIATA GITGOCGICC CAGGCICCGA GATAGCCCCA CATGATAAAT	60
30	TOCTATOCCA CATCATGICC TOGTIGICAT TGITGICCAA ATTOCTCAAA TCAAAAATGA	120
	AACTACCATC ATCTGGTTTC ACTITICAGIA AACTATCGTT TTTCTCTGTT GCAGGGTGGA	180
35	AATCCATATC ATCCCGTAGA TATTCTATGT ACAGCAGAAA COGAACCTTC TCTGCTGAGT	240
	TCAACACCTG AGCTTCGTTA GCAGCAATAT TEACAATTCG ATGCAGCTTG CCCTTCTTAT	300
40	TACOCCOCAA CAGIGIAGGG ATAICIACCT CAGCIGOCAA GICCCIATIC AIGATAGAAA	360
	CCICACCICT CAATGAAGIT AGGCGAGCIT CAGIGGGAAC TICCIGGAIC	420
45	TOGITICIAG AGCANICACA ANCIGONICI OGCAGOGGAN GINATTIGOC TICANGATIT	480
	TEATITTATE TETEOCTEAT AAACTOGAGE OCTOCAGET ATAGATETIT OCTOCATOCC	540
50	GAGATGTCTT COGTTTGTGG CTCTTCTTTA AATCATTGGA COGAGACTGC GTGATGCTAC	600
	CACTIOCATG CTOCTCCAAT GATTOCTGAT CCTTATACCA GTOCAGTGAC GTOCTGGATC	660
55	GAGAATTCAG ATOCAAATTA GOCATAGAGT TTGTGTATTC CTCTAGCTTA GCACCATCGT	720

	IAICITIOG C	731
5	(2) INFORMATION FOR SEQ ID NO:994:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 729 base pairs (B) TYPE: mucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1610UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:994:	
	GATOGATCTG TACAGAGCG TTACAACAGG CACTTGTAAA AAGCAATATC GPTACTTTTTT	60
30	TOCATOTCAG TITTITTOCTIC GAGCOTOGIC AGCOCGAGGA ATGAGTAATG GATACTITICA	120
	CGACAGAAAA AGTGAAAACT TTGAGCGGAC ATCGCAACCT GCTCGTTAGT AGCACCTAAG	180
35	COCAGOTTAG CACAATGOCG CCAAAGGATA COOCGGTGTC GCAGACCTCT ACGCGGTCTC	240
	GCTATATCAA AAAGGGCAAG ACTTTAGAGA ATGACATTGA GCTACAGTOG GTGACGCCAG	300
40	CCACCEGGGA GITICCCCGGAG GACCACACGG AAGAGGGCGA CIIACCAGGAG ACGGAGGICA	360
	AGAGGGGCT GAAGGCGCG CACATCTGGA TGATCGCCCT GGGGGGGAGG ATAGGCACAG	420
45	GOCTIGITICAT TGTGATTGCA TGCCCGCTGC GGACAGCCGG GCCAGTGGGG TCCCTGTTGG	480
	CGTACATCTT CATCGGTACG GIGGIGIACT CGATCACGCA GTCCCTGGGG GACATGGCCA	540
50	CGITCATTCC TGIGACTCCT CGGIGACGGT ATTTTCAAAG CGGTTTCTGT CGCCTGCGTT	600
	TGGCGTGGCA AACGGGTATA TGTACTGGTT CAACTGGGCG ATCACGTTTG CTGTCGAGCT	660
55	TICTIGTOGIT GOCCAGATCA TACAGTACTG GACGGACCGC GTGCCAATCG CGCCGTGCAT	720

	TGICATUIC	729
5	(2) INFORMATION FOR SEQ ID NO:995:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 666 base pairs	
10	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1611RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:995:	
	GATCCATCGT GGTGTCGTTC ATTACCTGTA ATTCCATTGA TATCCTGGCT ATGCAGTGCT	60
30	GCAAACGCTC CTCCAGCCCC TCTATTTTGT TATTCAGCTC CAAGTACTCC GCCAGCTTAA	120
	AGGICAACGA GAGOGACCCI GGAITIGCACC IGACGGOCGAI CTCAAGGACC IIICIOGIGCI	180
35	OGFTCTCGTC CACAAACATG GOGTAGTTGT ACCATATCTC CGGCGCAAAG CACATGTGCT	240
	GCACAGCCIG GCGGIGCACG TATTCCACGC GCIGGCGCAG CACGACTICG GGCAGGIGCA	300
40	GCTTGTTGTC CAGCTCCCAC TGGATGCACT TGGTGCAGAT CTGCAGCTGG TACTCATCGT	360
	ACTGACCOSG CGCAGGCAGG TRCTGCTGTG TCGCCTGGTT TAGCTTCGTG GGCAGCGAGC	420
45	CCCCCAGGCC CITCGICAGG TITCGACCACT CCTGGITACAG CGAGCCCCCA TICATGITAGC	480
	TOGOCCEAGAG CTCTCCCATG AACTTCCCCC CCGTCAACTG GTTGACCTCC TGCTCCCACT	540
50	GOGTGTATTT CTCCCAGTAC COCTCCAGCG ACTCCACTGG CAGOCACAGC AGGCGCTTGT	600
	ACAGCITGOG CAGAATCIOG ACCOGGCTOT GCTCCTCCCA CTTGCTCACC GGCTTCCACT	660
55	OCTOCA .	666

(2) INFORMATION FOR SEQ ID NO:996:

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 623 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1611UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:996:	
25	CATCHAAGOC ATGOCHCACT CCTOCCOGIG CTCACACCAC TCOCCACGIAG CTAGHAATGG	60
	TOCCANATOC ATCANACACC CTCCCTCTCC CCCTACACCC ACANACCACC CCCCCCCATA	120
30	CAAGITOCAG TICTACAAGC ACCIGCAGTT CCAGGGIACG AGGIACCAGG TGGTGACTTC	180
	OCCOCCUSTAT CTGATAGACC GGTACCOCCA GCCCAACGATCA GGTCGTTTGT	240
	CAAGTOCATC CATCOGAAAA TCAACGACGA TGTGACACGG ATCAGCGACG AGCGGGTGAC	300
	OCACODORIG TOGAAGIOGG AGAAGIOGAA GCIGTICCIG CIGCIGGIGA COCTGTOCCA	360
40	OCCOSSOSSI COSSAGIACT COCTOGACAA GACCAAOCOG TOCCAGAGOC GCOCCOSCOS	420
	AGACCIOCOCG COGAAGACCG ACCAGGTOGA GGAGGCCCCC AGCCGGCGGG GCCAGAGCCT	480
45	CGTCTGCACA CTGGTGGAGC AGATCATGCG CGAGAACATC ACGGAGGACT ACGACGAGAG	540
	COTOCACCAC GAGAACTACG TOTTCTOGTC GATATOGGCG AACTTCATGG AGGGCTTCAT	600
50	AAACCACTAC CTAGAGAAGG TCT	623
	(2) INFORMATION FOR SEQ ID NO:997:	
55	(i) SEQUENCE CHARACTERISTICS:	

	(A) LENGTH: 708 base pairs	
	(B) TYPE: nucleic acid	
5	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG161ZRP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:997:	
20	GATOCATOCG ATAAATCTOC TAGTOGTGIG GTTTCACACG AAGCAGCTTC CGTCGTTCTC	60
	GROSTTTTC CTGCAGCTCT GTTCGAGCTT GATTTTGGTG TTTTTGGGCA CGTGGACCAC	120
25	CAGGIGGCCC GAGCITCGCG ACACGITTIT TGAGGGICIC ATAGATCAGG AACCTATTAC	180
	GGGTGGGGCT GAGTCTCCCT ATCATGGCAG TTCTCAGAAC AGACAGCAGT TTGAGATGAA	240
30	GGACTTGGAG GCACAGAAAT AGCCTACATT ATAAATACGC TTGAGATCAT TCTAGCGCCA	300
	COGTIGAGACT GATCATTOGT AAATAGCATT TTAATAACGT AATATATCAT ACGCTIGGTTA	360
35	TTTCGGATGC AGGACTCCGA AATAGTCTGA CAATTATGTA CTGTTAAGTT ATTTATTTTC	420
40	AGACCIGCITA TCTCGCTTGA AACCTGTTCC AGTGCACAGC AGATCCAGCA GCTCGAATAC	480
	TGATTITTIC GTATTGTTAC CTGGTGGACA GATCTCCAAG CCACCCTCCA ATCGCTGCCG	540
45	CAGCIGCAGC ATTGCTACOG TAGACTOCAG OCTAGTGACA AGATGATOCA ACAAGGATAT	600
	CCAATOGIAT TOOGTGTTCT GGCTCAGOGC TTTATCAACC TTTTTATCAC GAGTCATATG	660
50	TGTGGGTAGT TGTAGGACAC TATTGTGGAT TTGGATCAGA CCGCCGTT	708
	(2) INFORMATION FOR SEQ ID NO:998:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 732 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEINESS: single

	(D) TOPOLOGY: Tinear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1613UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:998:	
	GATCAAATAG ATGTGCGCTG CCACATAGGA CGGAGTCGCG GCTAAGCTGT GTGTTTTACC	60
20	TOGRAGOCARC TOTTOGRACTIC CTIGTICTICAGE ARTICOGOGOGO COROCTOGOGO ARCIARGOGRAC	120
	TATATAACAA GOGAGGAAAC CACCITGIGA TACGCACGGG GACCAACGAC ACAGCAACGA	180
25	CACAGCAACG ATGGCGCACC TCGGGGCTCT TATTGACTTG ACGCGGATAT CGGAGACGCG	240
	GTATGAATCG ACGAACCATC ATAGGATGAT ACACGGCCCC AAGGCCCTCT ACGGGGGTCT	300
30	CCTACTOCCA CAGGOCATAC TOSCCTOCTT CTACTTTGTC CCCAGGCACT TTATTCCGCT	360
	CTCGGTGCAC TGCCTGTTCA TGGTCGGCGG AGACAATGCT ATCAAGACGC AGTACGAGGT	420
35	TGAACGOCTG COCAAGGGGA GCAACTTCGC GCACCTGTTG GTGCGCGCGT ACCAGAAGGA	480
	CAAGGAGCTG TTCACAATGC AGATCATCTA COGGGGGAC CTCGGCAAGC AGCCGGACAC	540
40	SCTSCACOSC AAGGACAACC TIGGSCCCTIGT GGACCIGGTCC CACCTIGGAGG ACGCTGGCAC	600
	SCTATGCAGG CGGGATCTAC TGTCCAACCG TGAGAACCTG CAGGGGGTGA GCGCGTCTTC	660
45	GAGACOGATA AGGGCCITAA TAACATICIG GAGGGGITGG ACAACAGGIC GICCGAGTAC	720
	ACCOCTGCCTG CC	732
50	(2) INFORMATION FOR SEQ ID NO:999:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 727 base pairs (B) TYPE: nucleic acid	

(C) STRANDELNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	, , , , , , , , , , , , , , , , , , ,	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1614RP	
15	(xi) SEQUENCE DESCRIPTION: SEO ID NO:999:	
	(va) Second Description: Sec 10 No. 939:	
	CATCOCCCC ATCCACCCCT CCTTCCACCC CCTTCTCCCC CACCCCCCCC	60
20	COCCUTACAC GACCACGICC ACCAGGICA COCCCCATG GAACAGITCC ACCAAGITCCC	120
	CGACACGATC CGIGICGACA AGITGGTCAC GTATATATIGG CGCCTGTTCG AGCCCCTCTG	180
25	COTOTIACCOCO COCCAACCAGO AGCOCTIGOCA TCTOCGAAGAC ATCATOCTCT TGCGTGTGTA	240
	CTGCCGCCAG GCCCGCGCCC ACCCGCTCTT GCTCATGGCG ATCGTTCAGG CGGTGGCGGC	300
30	ACCCTACCCC GICCAGACCC TOCTCTCCCA CCAGGTATTC ATCATCATTC ACCCCAAGTT	360
	GCGCGCGCA CAGTCATACT TGATGATOCC GCTGCGAGGG AACGCAAAGC CGCGCATCTT	420
35	CACCCCCCCC CCCTTCCTCC ACACTATCCC CCCACCACATA CCCAACATTC CCCACCCCCCC	480
	CASCETGEOG CICGCCCCCT TOCICACICC GCTCACGAAG CCCCCCGGFIG CTCACAAAAT	5 4 0
40	CTTCAAAGAC TGGTCCATCT ACTGCGACAA ATCCATATGG CGGACGATCC CTGATCACTC	600
45	GCCCAATGGC AFTCIGCGCT ACCTCCCGCA CTCCTGCACG CCGATGGACG AATCCATCTT	
45	TGAGTATTIC AUGICIAIT GGAAAACOGC AACAGCAAAC CACIOCACGA ACAACATTIT CCACACC	720
		727
50	(2) INFORMATION FOR SEQ ID NO:1000:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 726 base pairs	
55	(B) TYPE: nucleic acid	

(C) STRANDFINESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) OFIGINAL SOURCE:	
10	(A) ORGANISM: PAG1614UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1000:	
	GATCCTTTTC ACCAACAGCT GTCTGGGCCCA GCTGCGGCCCT GGGATGAGCT ACAACCAGGC	50
20	AGTGAAAGOG CTGAOGAACC TGGOOGTGGA CAGCTTTTACA CTGCCGGGGA CGGTGGGGTT	120
	TOUSCIGAAC AACSISTACT CIGISCOGST AGAGGACGST GCTCAGATGG AGCTGCTGAA	180
25	COCCIACCITE CACCACITICC COCCACGACCI COCCACCCCC CIGICIATICG	240
	GGCCGAGAGG GCACAGCCCT CGAAGTTCTG GCTGGCCCTTC ACAAGGCCCCA AGTTTATCAA	300
30	CAAGGCCCTG TAAGGCCGAAA TAGGTACGTA GCTGCCCGCCGCCAAGTA TTTACAAAGT	360
	TESCTETATE OCTACEAGET TITEGTESCE TETECCTTET TECACESCAC CACCACTTCA	420
35	ACCOCCAGE CICCCAGCIG TICCCCGTCT TICACCATCG CGTICACCTC AATOCTCACG	480
	TOGGTGTTTT TOGGGGGAA GCCTTGGATC CGCCTGCA GGTCTGTCAG CGCCTGGACG	540
40	ACACCCICAT AGICIOCATC TICTITICACG COCTCTTTGT ATGITTICCAA CCACTCACCG	600
	ATGICITOGA TACOGGGCTC GACTCTGCTG ATCATCTGCA TGCGCTGGGG CAACAGCTGA	660
45	TOSCOSTOSC TOTTOSCOTT COCOTOSCIA ATCATOTOCT GEATTTCOTC ATCOGTCAAG	720
	CCCGAT	726
50	(2) INFORMATION FOR SEQ ID NO:1001:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 704 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genanic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1615RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1001:	
	GATCATTCAG CTOGACCICA GCCCACTACT GTTGCACCCC ATATTCAGGG TCCCCCAGGT	60
20	CCACAACCAC ATOCTOCACA TICTOCOCCA GIATATOCTG CAGTOCOCC COCCGIACAA	120
	GCAGGETTIC CATGAGCTAT GCGGCATGIT CTACATGCAG CTTTACCGCA ACGGCTACCG	180
25	GCACGCATC CAGCACACCA COCTACATAT GITCAAGGAG TICATCGCAG AGGIAGCIGI	240
	GACCTTCTAC GACGAGGGAA ACCTCATOGA GTOGACGAAG AACACGTTTG AACOGATACT	300
30	TOGACACGOG TIGOCAGGOT IGIACGAGCA GOTTOTAATG CACCATGAGO TGGACAACTO	360
	CATATESCTC ATCOCCIGGA GCAGSCIGCT CTTTCTCCGA GAGTTCGAGC TGGAGTACAC	420
35	GCITTECTTG TESCATCACC TECTGACATT TAGATIACCCA GTATCCCASC TOSTAGCAGC	480
	CATTATOGIT GICIGICICA CACTCATTGI ACAMGAACIG CATTOCTGIG AAGACCACGG	540
40	CGACCICATG TCIATICTAC TOCACTACOC TCCTCGAAGC TCCTCACCGC CCCCACATCA	600
	TOOGCTOOGC COOGROCOTT CUTCATUTGT COUTCOCCCGA ACASTATGAA GACATGCAAC	660
45	TCATCIGOGA TICACIAATT AAGIOGCACA ACGGCGCCIG GITC	704
	(2) INFORMATION FOR SEQ ID NO:1002:	
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 706 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1615UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1002:	
15	GATCTCCTTA TICTGCACAA CATTGCCTAT AGGCACTGCT CCTGCTTTGT GTGAGCACAC	60
, ,	GIGIOCTEAC TITAAATAAG TACGATGAAA COGTCAGCCT ACOGTGGGGC CCCGTTTTTC	120
20	ACTITOCCAC GGAGAGGGTA TCAAAGGAGG TOGAACACAG CTACGTTATT GGTTOGTATA	180
	CONTOCTITIT CAAGOOOCTIA COTTICACCAG COCTICOCAGO ATCOCAGOCA COCCOCCOCT	240
25	ACCCCCAACG CCACCTCCCG CAATACCCCA GCCCCCTCCG CCCCTTTTCG TAAGTATATA	300
	TOOCCIOCOC GCOCCAGGICG CGCGAGGICGAC AATGCCTTCT CGACTTGACA	360
30	ACCIOCOGGA GEOGRICAGI CECCTOCAGA GCCTCAGCCA TAGACAGCTG CTCCGTCTGG	420
	COCAGGGGT GIGCATCCCT GCCCIGICCC CGTCCCTGCA CAAGGGCCAG AGIGGACGCG	480
<i>3</i> 5	TOTOCOTOCT COCCOCACTACA COCCOCCCC CHACTICACC COCCATICOCC	540
	COCCOCICAT COCCICOGAC CIGGIOCACO TOCIGIOCGA GIOCAACOCT CCAACOCCGA	600
40	TCAAGGOCTA CTGGCCGGAC CTGATGGTGC ACCGGCACCT GGGCGACAGT AGCTCCCTGG	660
	CGCGGGGGCT, GEYCCCCGCC, YCACAYGCCC, 1200GGGGCT, CG10CY	706
45	(2) INFORMATION FOR SEQ ID NO:1003:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 687 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(A)	ORGANISM:	PAG1616RP
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(xi)	SEQUENCE	DESCRIPTION:	SEQ	$\mathbf{I}\!\mathbf{D}$	NO:1003:
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40 45

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GATCIOCTIC AA	GAGCTCCT	TCTGGTAGGA	CCAGCCCAGG	ATGAAAATCT	TOGAGACOGT	60
CACAGOGICC AG	GAACOGCT	TGAACAGGGG	202000TAAD	GAGAAGCCCGA	ATGGCCCGTT	120
GATCATGTAG AA	CTTGCCCA	T0002T003G	GIAGIAGITC	TGGCCGATGT	TOGAGGOOTC	180
GCGCACGTAG CT	GAGCACCI'	GCGCGGCTGC	GGAGATGGAG	AIGCCCTTGA	GGTCTAGGAT	240
GETGCAGGAC GT	CTCGACGA	GOCAGTOGGC	CIGICIGGAG	CIGGCCGGCA	AGCGGTACCG	300
CGAGAAGGAC TO	GTACTCCC	ATATCA A GTT	CTTCAGCATG	CCCTCCTGCG	TOGIGATOIT	360
GTACATCTCC GT	CAGGITCA	00000000AG	CTCCTCGATG	TACACCEGCC	TCCCGTCCTT	420
CICCOICITG TO	GIAGIACI	GCGGGTIAGAA	CTTGGCCACC	AACGGCTTTT	CCTCCTAGTG	480
GAAGTCCTCG AA	GATOGTGT	CCACGCCGTT	TTCCTTACGC	CACTTCTCCC	AGPTCTCAAA	540
CATTOCCCCC GC	AGCCGCCC .	ACGITICGAAC	TTGCCCCCCCC	GCAGAAACCG	CAAAAGCCTC	600
CACTOCTOCA CA	CCCTTCGT (GAATCCGGCC	TOCTTCAGCA	CCTTCCCCAG	CTCCTCCA6C	660
occoccioce io	creasere :	CCTCAGG				687

(2) INFORMATION FOR SEQ ID NO:1004:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1616UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1004:
10	GATCACCITT TGGCACGAAC GCCACAGAAA ATCCATTACG CGATTCTGCC CGTTCATTTC
	TETACGAATG GOGAAATGAC TOGTCGCCAT GOCACAGGTG ACTATCGCAT TTCGTTTCGG
15	GGGCGTCATC CCCAGATTTT CTTGCAGAAA GCCGCCACCC TGCGGGATAG GGCTTTACCT
	CACATGAGOC GCAAAGOGAC AATAATOGCA GAGCTGCTTC TEACTTCATT CICTACCOCA
20	CTAACGTAAT CGATCOGACA GOCACAGTCC TACOGTAATC CTCTGAGATA CCAGATTOOG
	TIGCATAAIG ATCTCCCCTA CAGGGCCGIG TTIGITCGAG CCCATAICIC AIGCAAGAIC
25	GCGATGCCCG TGACGATCCA CCTTCACCAT TTACTCGTTT CTTTTTCAIG TTTTCAAAAA
	GAAACGAAAA OGTGAGATAA AAAGCAAACA TTACTACOGA CATTTAAAAT AGGTGATGTC
30	CASCACIGIA CCTCATTGIG GGCGCTAACA GCACCAGCAA TGTCTGIGIC ACCCCTTGTG
	CTGTTTGACT TTTCAACAGA CAATOOGAAC ACACTGCCCC GOGAATACGA CCTTGCAGTG
35	CCCCGAATCT GTGTGCTGGG CCACGGGGGC AGTGGCAAGT CATCACTGGT TGCTCCGGATG
40	GCTACACGGA CTGCAGAGTG GCCTG
40	(2) INFORMATION FOR SEQ ID NO:1005:
	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGIH: 703 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDELNESS: single
	(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1617RP

	(XI) SECURICE DESCRIPTION: SEQ ID NO:1005:	
5	CATCHIGACA CCAATOGACT TOOGGAACGC CTGAGTCAAG GCCTGGGTCT TGGATAGCTC	60
	CAACGAGAAT ATCTCTGACC CTGCCATCGC TGTGAAGGGC ACATCTGCGC CCAGTGACTG	120
10	CGACAAGCCC ATCGCCAGCG CCGTTTTGCC GGTCGACGGC GGACCAGCAA CCAACACGCC	180
15	CCCCCCCCCA AUGUIACOGT TCTGCACCAT TTTGAGAATC ACGCCTGCGG CCCTCCGCCC	240
	CIGIPACIEG COCACCATTO COIGCGASCT CGGCPTAGGC TGTAGGITCT CGTCCAGTCC	300
20	CAGGOCAACA ATGTGCGAAT GIGTGGCAAT TAGCGACAAG GACTTCAGAG ACATGTCATG	360
	COCCIOCIGI GITTGAATCG ACATATTATA GATCITTGAA ACTITGAAAC OGICAAGAGA	420
25	GICCAAIGGC CITIGICGAT GACCGICTAA CIGITCAAAC GGITGIGCAA CATACCAAAT	480
	THTCCCGCAG CCTGAGGACT AAAACGCATG TTATACGAAG TCAAGAAGAA GCATCGTITG	540
30	ASCRICTAGE AGRICULTICA CTETEAACTT GGTGCGAGCG TGCGGTGTGA TGCTTCGCAT	600
	GOCACAGIAC ATATOTOGIT GCAAGCCACT TIGGAACCTG TGGGCTAACG ATGTACGCAT	660
35	CACCGTGAAT GGGAAGCGGT ACTTGGTGAC TGGGCTCCTC AGT	703
	(2) INFORMATION FOR SEQ ID NO:1006:	
40	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 696 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
60	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1617UP

	(May object blacker rich). She in No: 1006:	
5	GATCAGTTCG TCGAAGAATT CATGTCATCC AGAGAAATCG GAACCAATTT ATGCTCACCT	60
	COCTOCCCCT GITCTCTTTC TACCGCCAGG CCATGCAGGC ATGTCAGGCG CTCAACACAC	120
10	CHAGIGACAA ACTOGOOGHT GHOCHGACAG CCHATGOGHT OGHAAATGIT AAGGOCCATCO	180
	CATGITICGAA GAGGIGACAG AAATTOCCGC TGTAAATTCT CAAAGAAACT GTCCAAGGCC	240
15	GTATCCTTCA CAAAGTCGGG GCGCCCCCCC AGCACATCTT CCAGCTTCCT CTGTTCCCCC	300
	GAGGCCTTGC TCATGCTCGT GGCCATTGCA CTTGCTCAGC TCGGCCTCTG CAAGTACGTA	360
20	ATTITAGCTA TOGAAAATTI TOOCTOCTOG OGATGAGCTC ACGAAGTCTA CATACOGATT	420
	GACTAAGACA CTTGCCACCC GTTTGCCCCCT CATGCCCACTA CACCAAGGAC CTCTGGACAT	480
25	CGAGGATCAA CTTGCCCATCA TTGCCGCACCC CCCCATAGCC GATCTTGACA GCCTCAAGCA	540
	AATCTTTTCC GAGCTCATCG ATCCAAAGCT CCTGCCATCG TGCAGCGACC CAGACACGCT	600
30	CTGCACGCCG CTGCACATGG CTGCCGCCAA CGCACACGCC GACGTGGCGC GCTAACTGCT	660
	CTOSCISCIC CACCOCCCG COCCACCCA CTOCCG	696
35	(2) INFORMATION FOR SEQ ID NO:1007:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 360 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(a) Island	
95	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
5 <i>0</i>	(A) ORGANISM: PAG1618RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1007:

	CHICCOCCAL CCACHARMAC MOCLIMICCA CAMERCIAC CHAMORACA CAMICOCCOC	60
5	CCCCCCAAA AAAAAAACCA TGAGACTCTG TATCAGTAGG AAGTCTATCG CATCTTCTTA	120
	TTTAGCCTGT ATATGTCCTT TCCGCGTGTA GACAKTGCGT TCGACGAGTA TGCTCGATGC	180
10	GGAATATAAC GI'ACTITTITI GAAGAGIAAT ATGGACTITIC GACCTOCAAA GI'ACCGI'CTG	240
	COSTIGUEST GIVAGACACT CATCOGRANCE CARTIGITICS COCRTCACOS TATOCITICIS	300
15	TIGINIGCIA TOGIAGCINI AGOGICIGGA COOCTAICCA CACAGATAIT ATCCCATTAA	360
	(2) INFORMATION FOR SEQ ID NO:1008:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 637 base pairs	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1619RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1008:	
40	CATCAACAAT GTGCCGCGCC TGCTCCTGTT CCGCCCGGCC GGTCATCTGC ATACCTACCA	60
	GCCTCTCGGG ATTCCGTCGC ATACAGGGGG CGCACGGGTG CGGGGGATCA TCGACACCCT	120
45	CAAGAGTTAC ACCOGCATOG AAGACTTOGA GTACCACGAA CCAGTGAACT GCCCCAGTA	180
	TOCCOCTATE CICATGATES COGTCCCCCT ASTAATCATG CTGCGCAACT ACTGGTCCGT	240
50	TGIGGIGICC ATCGCCCTTT TCCGCCCTCT GIGGGGGTTC TCCTGCGTGT CGATCGTCAT	300
	OGCACTIGIG AGCOGCOCCA TGITICAMCAA GATTAAGGAC ACTOCCTAGG TGOGCTOGTC	360
55	COGTIGATIGOC AATTACGTICC AGTACTTCOC AATCAGGCAG CAACAGGTTC AGTTCOGGGT	420

	GGAAACTCAA ATCATCTOCG TCATATATGG CACCCTCAGC GCAGGAGTCG TACTACTTGC	480
5	CATTOGCACC AAAAGCATCA GAGCTTACTA CATCAAGTAC AACTATAGCA TGCACGOGGT	540
	GGIGCACITG TIGHTGICCC TOGCCGCAAT ACIGCITIATC TATATCICCI TOGCCGCCCT	600
10	GCTCGCAGIC TTCAAACTGA AGAACTTTGA GIATTCA	637
	(2) INFORMATION FOR SEQ ID NO:1009:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
00	(C) STRANDELNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
25		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1619UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1009:	
35	CATCOCTTGC TGCAGACCAC ACATTTTICTA GOCTTGTGGG TAAGGGGGAG ATGGGGTGGA	60
	CAACCACGGA GGAAAAGCTC ATGAAGCTGA ATCCAACAGC TACAGATGGG AACAATTACA	120
40	TTAATACTGA TACCACTGCG AGCAAGCCGG CTCCACCTTC GTCAACAGAG GCTGGACAGG	180
	CAATTGAACG AGAAAAAAA CTAGACCGGA GOCAGACTGA GAAGGACAGT GTAGAGACCA	240
45	GCAAGGITGA GCGCCCGGTA GTAGATGCAT CGTAGGTAGG GTGGAAGCAA ATCGGCGGGT	300
	COCAACACOC CCACCCACTC ACCCAACATG ACCTGCACTG CCACCTTCAC ACACAAACCT	360
50	TTITAAGCCA TGTGCTGCCT GCTGCTGCGT ATGGCGACTG GTATCACTCC GTGGGGATAT	420
	TOTTOCTOGG OSCATTITTEA TOGITIGOGT TOGGCTACTT CAAGITCAGT TIATCACCTG	480
55	TATTCITOGT AATGGTTTTG ACGCCTTTGC TATACCGTAC ATCGATTTGG AAGTACAGAG	540

	GETOGATAAG GGAACTOGTG CAGAAGGAGC TCACAGTGCA GAAAGTAGAG CATGACTACG	600
5	AGAGCATGGA CTOOCTCAAT AACTTCTTGG ATAAATTCTG GACCAGAATA GAGCCCAACA	660
	TITCCGIGAT GGITGIGGAT CAGGIGAACC ATGAATTGGC TAAGAACCGT CTGTGCCCGG	720
10	(2) INFORMATION FOR SEQ ID NO:1010:	
	(i) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 664 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20		
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1620RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1010:	
	CATCAAACTA TITCTTGTTT TGTTGGTGCA ASCATACTTT CGTCAGTACT AACTTCTTCG	60
35	CTCCACTOCA TAAATTOGTA TTCCCTATTG GCATTAAATT CCGGACCCAA GGTAACGACC	120
	AAAAACATTA GAGCAATAGA TCCCCACACA AAATAGGCCA TAACTCTACC ATAATCATAC	180
40	AATTCTTTAT TOCCATTATC CAGTCCAAAA TTTCTTCCAA GOCTOCTTTC AAGCAACCAT	240
	GAGGGCTAG ATGCCAAGIT TCCCAATTGA TATGCCAGGC CCACGAAAAA GGTTTTCGTG	300
45	TCTGAGTTTG GAGCTAAGCA GTGTAAATGA TGTGGGACAA GGCCCCATGC TCCTTGAACA	360
	AAAAACTGTA GGAAGAACAC GGACACTATA ATACTTCTAT CATGTACAAA TCCCCACGGA	420
5 0	TAAACAAGAC AGGCAGCCAA CAAAATACAC ACGAGGATAA CAACTCTTCT AGAGCTTATG	480
	CTOGRARAC GIGRARATGRA REGICCACCT RITRIRGCAC CRACGITGGC TOCRCRATIT	540
55		

	GIGALOSCIG ALIGATIOSS ALAMIANCA ASTIGITAN ICASCATOS TOTALAGACA	600
5	TCTTGAGACG CATGAGAAAA GTAATTATAA CCCGTCATAA GCAATATCAT GTAGATGACA	660
	ATGT	664
10	(2) INFORMATION FOR SEQ ID NO:1011:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 727 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1620UP	
25	(A) CROANTSM: PAGIOZUUP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1011:	
30		
	GATCAAATAA AAATAGAAAT TAGCTTAATG GTAGAGCATT CGTTTTACAC ACGAATAATT	60
35	TCAGFFCCAT TCTCAAATTT CTAAATAATA ATTAACAATA ATTFAAATTT GOGTAAAAAT	120
35		
	TAATAAATAT TAACGTATAT AATAATTATA TACTITATAA AATTACTCAA TGITATTAAT	180
40	AAATTTATIT CTIATCATTA ATAATGATGI ACCTACTOCA TATAATATAT ATTTTCAAGA	240
	TICACTACTA CCICATCAAG AAGGIATTITI AGAATTACAT GATAATATTA TATTCTATAT	300
45	GITACTIGIT TTAGGITTAG TITCTIGAAT AATAATTAIT ATTATTAAAG ATTATAAAAA	360
	TAATCCTATT CTTTATAAAT ATATTAAACA TOGTCAAATA ATTGAAATTA TTTGAACTAT	420
		4∠0
50	THE COASCE ATTATTITAT TAATAATIGG ATTECCATCA TITATTITAT TATATTIAIG	480
	TGATGAAGIT ATTTCACCAG CTATAACTAT TAAAGITATT GGIPTACAAT GATATTGAAA	540
55	ATATGAATAC TCAGATTITA TTAATGATAA TGGTGAAACT ATTGAATATG AATCTTATAT	600

	AATICCIGAA GAATIATIAG AAGAAGOGIC AATTAAGAAT GITAGATACT GATACTAGTA	660
5	TIGITATICC TOTTGATACT CATGIAAGAT TIATIGITAC AGCTCCTAGA TGTTATICAT	720
	CAATTIT	727
10	(2) INFORMATION FOR SEQ ID NO:1012:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 665 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1621RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1012:	
30	(X1) SECONCE DESCRIPTION: SEQ ID NO:1012:	
	GATCCACCCA COSTIACCIC CIACTIGGCC GIATCIGCGT CTCCGIGGCG CTTCCCCCIG	60
		•
<i>3</i> 5	AGATOCTOTO GOCCCGAAAT GIACTICTICAA ATGGGCTTGT TCAGTGGCCC ATACACCTCA	120
JO		
	TTAAGCTCAG TGGCCCCGAT GCTTAGTAGT AGCTGCGCCG CTCTTCATAC TGCTGTCTTG	180
40	TATTATTCAT CTTCCTGTAT TTTCTCTCTG TGTCCCCTCA CCCCTGCAGG GGGGACTGCC	240

	TESCECCOCC COCCUCTOCT COUTTCTCCT CTECTETGAA AATCGACAAA CTCCAAAAAA	300
	TOGASTITOG COCCCCCAC AGITGATIAA GCTCCCCCAT CTCTATTCTC TATAAATTGT	360
45	TOTAL TOTAL TOTAL TAN OCTOBOLAL CICIATICIC INIMATIGI	360
	TAAATTAACC ACACTGTGAA GCCCTGCAAT CCGCACGCCG CCGCACGTCA ACTCTTGGTC	420
50	ACAACCTAGC CCGGGGAGTG CAGTCTCACA AATACAAGGC CTGGGATATC ATGTACTGAG	480
	GOCTOCTIGAA CGTTTTCCCCT TTTTTCTAAA ATCGCTGTTC ACAGTCTTAG CGCAAAAAAA	540
55	ATAATTIAAA AAAAAAATT AAACTCTTAG TGAAATGAAA AAATAAAATA	600

	CCASCIOCAS AACACCICIT CAAAGCATAT AACTAGCATA COCATAAACA TATOCTIGIA	6 6 0
5	TACTC	665
	(2) INFORMATION FOR SEQ ID NO:1013:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 666 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDETNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1621UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1013:	
	GATCTCTTGG TTCTCGCATC GATGAAGAAC GCAGGGAATT GCGATAAGTA TTGTGAATTG	60
30	CACATTITICS TOWATCHICS AATCTITICAA COCACATTICS GIOCTICIGGI ATTICCAGOGG	120
35	GCATGCCTGT TIGAGCGTCA TITCCTTCTC AAACCCTCGG GTFTGGTAAT GAGTGATACT	180
	COGTOGTAAG ACAAGGTTAA CTTGAAAATG CTGGCCATGG GCCCAACTTG CCCCGCACTGC	240
40	GETCTGAGCT AGITTICTACA CTGGGIATTA GETTTGGAGC AGATGGTGGA GTGGAGCTGG	300
	COCTTGAAGA ACCTACGACA AACAAGGCCT TOCAGGCGAA TAGTATTCCC AAAGTTTGAC	360
45	CTCAAATCAG GIAGGATTAC COGCTGAACT TAAGCATATC AATAAGCGGA GGAAAAGAAA	420
	CCAACCOGGA TIGCCTTAGT AACGGCGAGI GAAGCGGCAA AAGCTCAAAT TIGAAATCIG	480
50	COCCUTCES COICCOACIT CIAATITCAA CAAACIACCT TOOTTOCIAG TOCCIGICIA	540
	TGITOCITOG AACAGCACGI CATAGAGGGI GAGAATOCOG TCTGGCGCGG GTGCTAGTGC	600
<i>55</i>	CATCTAACCT TCTTTCCACG ACTCCACTTG TTTCCCAATG CACCTCTAAC TCCCTCTAA	660

	ATTCCA	666
5	(2) INFORMATION FOR SEQ ID NO:1014:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 676 base pairs	
10	(B) TYPE: mxleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1622RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1014:	
25		
	GATCOGIGIA TITTITTATTI ACATTATTIA ATTAAAAATA ATGATTIAAA TAAATATTIT	60
30	TTATAAAAA TAATTAGIOC ATTGTTACAT GITCATTAAA CAATGATTAT TATCAAAACC	120
	ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTCAC TTAATTAACA ATTAGGAACT	180
35	TTATCTATTA GICIOGGCIG TUTCCCTTTT GATTATTAAC CTTATCGCTA ATAATCTGAA	240
	ATATHTAATT TTAGATTAAT AATATATTCT GAGATITAAT ATTTTTAATA AAATAAATAA	300
40	TTATTCCCTA AATAATATTA ATAACTATAC CATATATAT	360
	TAACATATGI TIOGTAGAAA ACCAGCIATI TOCAAATCAG ATTIGACTITI CICIACTITAC	420
45	CATTATTCAT CACATAATAT TOCTACATTA ACCIGITCAA TOGITITIAT ATTTEATTAT	480
	ATTITIAAATA TAATAAATAT ATATTITAAT CATTIGATAA TAGTAAGATC ATCTGCTFTC	540
50	GOGITAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTAACAT TGTTAAATAT	600
	TIATATTATT TITAATATCA TITITTATTI TAATATTATG CIAATATTAA TIACITOCIG	660
55	ACCCATTATA CAAAAG	676

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(2) INFORMATION FOR SEQ ID NO:1015:

5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1622UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1015:	
	CATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTTAA	60
25	CAATAAAATT CAATAATTIA TTYAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
	CHIPPETI CHIMITA TIMENIMA GILIPETINA TOLUMINI IEELIMINI	120
30	TATAATCAGA TATATATTIT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAAITTG	180
	TOCCAOCAGC TOCOGTAAGA CAAAGGGGGT TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240
<i>35</i>	GIAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300
	GIAAACATCA AATAATAATT ATATCAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
40	TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATGG GATTGGATAC COGAGTAGTT	420
	TIACCAGTAA ACAATGAATA CCTATTTATT TITTATTAAT TAAAGAATAA ATTAAATGAA	480
45	AATTAAAGTA TTCCCCCTCA TGACTACGTT ACCAATAATA AAAATCAAAA CAATAGACGG	540
	TTACAGACIT AAGCAGIGGA ACAIGITATT TAATITOGATA ATOCTOGATA AATOTTACCA	600
50	TTTTTCAAT ATTTAATTAT AATAATTTAT AATTAATT	660
	CAGTTOGROC TOCAAAGTIT TAGAATTIAT CATAAACGAA CATAACTCTA AATATTIT	718
55	(2) INFORMATION FOR SEQ ID NO:1016:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 747 base pairs	
	(B) TYPE: nucleic acid	
5	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1623RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1016:	
20		
	GATCACAAIC GCATGGTATG ATCGTTTTAG AATCAACGAA ATATGACAAA ATGAAGGAAC	60
	ATATTOCCAT AAGGACTICA GGIATTACAG TOCCAGATAT TOTATOCAAG TOCCACTGAGT	120
25	ATGGTTTAGT ACCTATACCA AAAGAACAAT TTCAACAGAT TAAAATGGAA TTAGAGCATC	180
	CAAAGITTAC TAGAGAGATG ATTGTTGACC ACOCTOGTGA CTTCGACTTA ATTGCAGTGG	240
30	AATTAAAGGA ATACAATOOC CICAAAAAGC AATCOCAGIT CTCCTTTOGT GACATTITTOG	300
25	ATAGCATTAA CACTGACGAG GAAAGTGAAG CATCTGATTT TGAATATCAT GATGACGAGA	360
35	TARAGCACCT TARCARGACA GOCARACOCT TTOOGITATT ATGIRTTOCA GARGCTGOGT	420
10	TTATOGCTAC TTCCGTCGCT AGCACGCCTG ATGTCGATAA TGTCGTCGTG CTACCAATAA	480
10	CCTACTATAA TAAGITGAIT COCAATGAAG CAAAGAGOCT CGAAAAGCTG ACTGACTGGG	540
45	ATCITCAGIC AGAAGCTAAA AAACGTGGCT ATCATATAAA TITCAGCTTC CAGAAGGAGG	600
••	ACCCCCACC COCCCCTTCA ACCCTATGTC CTCCACGGAT CCCGAAGTTT TCCCCAAAAC	660
50	CGITCGACIT TGTCACTAGA CTCAAAAACT ACTAGAAGGG CGITTAATGA GGCTGCTACT	720
	GTCGCCGCAC AGAGCGAATT TGAACAG	747
55	(2) INFORMATION FOR SEQ ID NO:1017:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 758 base pairs	
5	(B) TYPE: nucleic acid	
3	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1623UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1017:	
20	GATCAGOGCA AAACACATCT GTATTCOCCAG CAGCATGTOC TOCTOCCACCT GCCGCATGGC	60
25	CTGGCTTGCA AAGCCGTCCA CCTCGCCGTC AAATGAAATG	120
	TITOGCAACC ACAGGGITCC CGIGCIOGIC GIACICCIGI TOCICAICCI CCICACCIGC	180
<i>30</i>	CTOSTCTOCC COSCOCACGT CCCACGCCCT AATGCTCAGC TGCGCAGGCCT CCTGGGCATA	240
	CCGCTCCCGC ASCGTAATGT CCACCACCAA GTGCTGCTCC TTGCTCATCG CAGCCGCGT	300
35	GAATGAAGAG CTTGCCAGCG GGATCAGATC CAGTTTTAGG TCCACTTCAA ACTGGATTTT	360
	CGGGTACTCC CCGCACACCA CCGTCAAGTC ATCGGCATAG ATGGACTCAA GCACTTCCAG	420
40	CICCIGCITT TECTCCTCCT GATAGICCAT ACCIATOGC TOGACCAACT AIGAGOCCAC	480
	GCGCAGCTTA GGGCTAGACC GTTACAGCTG CAGGTGACCG TCCGGGGGGAC GATGCGCTAT	540
45	COCTOSCICAA ATTITITOSCC TATACCACCA CITTATGITTAC CCGGTCTATA GIGCTGCTCT	600
	COGACCICAC TGATGGTGCT GTCCCGCGGG GACTGCTGCC TGGTGCGGGC AAATCCCCAC	660
50	COCTOTOAAC GOTOGITOCA TOTOCGICAC GOGTICACOG AACGGGAATT GOGCGCGCCC	720
	AGAAATCITG GCGAACCATG CTGCACTTAG CCTTACTG	758
55	(2) INFORMATION FOR SEQ ID NO:1018:	

	(1) SECONDE CHARACTERISTICS:	
	(A) LENGIH: 690 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1624RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1018:	
	GATCGCACGT CATTITIACCT ACAGGCTGGG CTTTTGAAGA AGACGCCTGC ATGGTACAAT	60
25	GICGIAGUCA GGATOUCAGU TGIGACUAAG TIOGCUAGAG AACOGAAGUI GUAIGACOCA	120
	GITAGOGGCA AGTACAAGGG CGAGCTGGAT ATAATGACGG ATAGATTAAA CAGAAACACA	180
3 0	GAGACGTACA AGACACGOGC TOSGAGTTOC GACCOGCAGA CGGCCGGGGT GCACAAGCCT	240
	TCTAASCIGC GGTTTAICGA GGACAASCIG CGGICGCIGT TTTTCCAGCA GCAICCCIGG	300
<i>35</i>	GAGCTIGTOGC GGCCGAAGGT GCTIGGTIGGAG AACATGGGAA ATGAGCAGTA CGACTGGTCG	360
	COGATETIEC ACCIACICAA GOOGOTIGAC GETGAGICIG TOGIGCAGOG GACOCIGTAT	420
40	CTOCTGAAGT COOCCOCCA COOCGAGATG CTGCCCGCCAT ACGACCAGCC GCCCTTTGAG	480
	TTCTATCSTC TGAGGATGCA GCAGGAGCTG GAGGAGCAAA TAGGGTAGGA GGAGGCCAGG	540
45	ATGGITGGCG CTGTGTTCAA GACAACCGCT GTGGAGCACG GTCTGCAGCA AGAGCAGAAG	600
	GICCICCACA AGIGGAAGGA GGACGIGGIT GCGGGGTIGC AGCIGAIGIC IGCCAAGAAG	660
50	AACTCTACAA AGCAGTCGTG GGCCGAAGCC	690
	(2) INFORMATION FOR SEQ ID NO:1019:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) ITATIL. 7/2 bace pains	

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1624UP	
15		
13	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1019:	
20	GATCATATAT CTTCCTGTGG TAAGGTCTGT GGGAAGCAGC TCTCCTGCGG GAATCACACT	60
20	TGTCCCATCA CCTGCCACGA TGGTAACTGC ATGGATCCAT GCCTCGTTAT AACTGAGCAG	120
25	AAGIGIGCAT GOGAACAGAG GOGITIOCTT GTTOCTTGOC AGTTOCCCCA TTOCCCAAGT	180
25	TOCACTOCAA AATGTGAATC ATTGATGTCT TGTOGTOGOC ATCGGTGCGC TGAAACATGC	240
20	TGTTCCCGGTA GACCCCATTC TGTCAAGCCG AACTCTAGGC GGCCCCGTGA GAGTCCAGAT	300
30	GATGAATCIG AAGTIGAGGC CCAGCACGIG TGCTIAAAAG ATIGIAATCG GGIGCIGCIT	360
	TGTGGTATCC ACATGTGCAA TTACAAATGC CATGCAGCA AATGTGCTCC CTGCTTACAA	420
35	TCAGATICCA ATGACCTIAT CIGICCCIGT GGTAAGACAA TOGTACCAGC COCIGICOGT	480
	TGTGGAACAA AGCTCCCTCG CTGCACTCAT CCATGTCGAA ACTCGCTGCT GGATACTTGG	540
40	CCCTCCCCAC ACACTCCACC TITCCCATAAT TGTCATCCCT TAGATGAACC TTGCCCCCCA	600
	TGTACCATCA CAGTCAAGAA AACTTGTOGC TGCGGTAAAA ACGAGATCAG GACATTCTGC	660
45	TACAATGATG ATGTGTGGTG TTCGAGACCG TGTTAGAAGC CATTGTCCTA TTGCAATCAC	720
50	TTCTGCCAAG TTCCCTGTCA TT	742
50	(2) INFORMATION FOR SEQ ID NO:1020:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 725 base pairs	

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1625RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1020:	
20	GATCAACTAC GAGGACTTGA CGACCGCACG ACGGGAGCTC GCGCCCGCGC TGGCCACTTT	60
	GGAGAATATG TAGCGCACAA CATCAGCAAT GITACAGTAC ACACGICIAT COGIGGGGIA	120
25	COSCTATGAT GAATAGAAAT ATATACACAG CIGOCTGCAG GCAGCTTAGA AGOGCAGAGG	180
	CTIGGGUTIC TCCCACGAGI ACTCCTGGIT AGIGAAGIGC CCGTACGAGG CGGTACGIAG	240
30	GTACATGGGC TTGGGGAGGT GGAGCTCTTT GACAAGAACA CCTGGTCTGA GGTGGAAGTT	300
~	GITECGEATE ATCTCEATEA ECTOGICGIC GEACTTOGIC CTEGIACCET AAGTCTCGAC	360
35	GIGGATGGAC AGGGGCTGGG CAATACCAAT GGGGTAGGCA AACTCAACCT GCACACGCTT	420
	GCACAGGOOG GOGGOCAACA GOGACTTGGC GACCCAGGOC GCAGGOGTAGG CAGGOCGAACG	480
40	GIOCACCITC CAATAGICCT TICCOCACAA COCACCOCCA COCACCOCCG COCCACCOCC	540
	GIACOCGICA ACAAIGATCT TICTACCGGT CAGACCTGCG TCACCTTGTG GCCACCGATC	600
45	ACCAAGUSC CCAAGGCTGC AACTAATACT TOCTGTTTTC GTCTAGCATG TOGGCAGGGA	660
	TGACCTTGCC TACGATGCGA TCGCGCAACG CGCAACGCAG GTCCTCGGTC GACATGTCGT	720
50	cccccc	725
<i>50</i>	(2) INFORMATION FOR SEQ ID NO:1021:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 726 base pairs	

	(C) STRANDELINESS: SINGLE	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1025UP	
15		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1021:	
	GATCTOCCTC TGCGCCATCC CAAACAACCT GGGTGTTGAC AAGAAGTACT ATGATCACCA	60
20	CAAGAAGGAA TGGGCCATGT ACCAGGAGAT GATGAAGCAC TATGCCAACG AGGACCTTGT	120
25	CCACACCAAC ATGCAGGGG GGTTTATGGT CGGGGGGCCA CTCCAGGAAA TAGAGCTGCA	180
25	CAACTTOCAG CTCGGCGTCT ACAAGGAGCT CGTAACTAGC ATGITCCCCT GACTTCATGG	240
30	AGTOCASCAT CGCCCATGIT TTATGCCCAA TACTTTTGAG ACTATACITA TATTATATAC	300
	TGATAAACAA TITCCCCCCC TCTCTCACCC CCACTACTIG TICTCCCCCGT ACAACAACIT	360
35	CACOGOCATO AACTOCAGOT TOTTOTOCO COCAAACTOG COCACACOCA CAGOGOCOCG	420
	CTTCTCGGTG TAGCCCCAGT TCACGCGACT CTGCAGGCGG GTGACCTCCT CCTCGCTCAG	480
4 <i>0</i>	TTCTAGCCCC CCCCCCCCC CAAACAACAA CCACACGTAC CCGTGAGCCC CTGTGCCCCCC	540
	COCCOCCACA GOOCCATCT CCTCCACCIC COCCOTOCCC TTTACCACA CCTCCCACAC	600
45	CCCGTCATCC CASCCCAGOG TTATGTTCGT TTCCAGAAAG TCCCAGTATT CCCACCACTT	660
	GIOGIOCGAE COCCACOCAG CATCIOCGIC IGICATOCCE ACOGIGAATA CGICCCCICC	720
50	CTGACG	726
	(2) INFORMATION FOR SEQ ID NO:1022:	
55	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 643 base pairs	

	(C) STRANDELNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1626RP	
15		
,,,	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1022:	
20	GATCOGTOGG GACCATIGOGC AGATGGOGGC CTTAATATAA GCCCCTCCTC GCAGGCATGA	60
	CGTCTGCCAA CTCCGACCAT TCTAAATGGC CAGCTGCTGC TTTGATGGTA GCGTCCGCCG	120
25	CTGGCGCAGA AGTAAATATA GCCATTAATT CCCCTTCTAA ATATACATTA CATACCAGCG	180
	CTOCAGAGGC GUTCOCGAG CGCTCCCCGAG GCCACGCCGCA GCCACGCCGC	240
30	TECCAGCTEG COCTCTEGECC ACCCAGACAT GOOCCCCCAC CCCCCCCACCT TATATACACC	300
	CTGGCCTGTC TCATATGCAG ATGGGTCTGA GCGAAAGAAG TTCCTGGCTC TCGCAGAAGC	360
35	ACTOCTOCTIC ACCOTOCOCC TOCOCOCCA ACCOCCACA ACACAATICTT CCAGCCCTTC	420
	COSCOGACOC GCACTOSSOG TACCOGTISCA GGTAAGGATA CTTOSSOGGC GCOSGGGCAC	480
40	CACCIGCOCTC AGOCTGACTT GOSCAACIGG CATACICAGA GGACCOGOCT GOCTGODOGC	540
	TITICOTOCCT GTOCACGTCA TCTCACCGCC TGCCTCAGCC GCCCTGGTCA ACGATGCGCA	600
45	CCAGACCCTC CAGAGCGTIGC CTTCGTIGCCC AAGTCGGAGC CCA	643
	(2) INFORMATION FOR SEQ ID NO:1023:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 704 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1626UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1023:	
15	GATCCATOCA TATTIGCGAA CITACGAAAA AAGOCGIGAA GAGOCCGAAC GIAATCIAGG	60
	TUTOGAAGAA TUAATGAATG ACAACATAGA CCUTIGUTACA GGAGAAAATA ATGAAGAAGG CCAGCUGAAA CAAAAGAAGT TGUTAGAGGA GCAGUTGGCA AAGTUGGAGA AATCAAAAGA	120
20	AAGACGACAA GUACOCAAGG CCGCGAAGGA GAAGAGCAAA GATGOCAAAG TCGTGAAAGT	240
25	AAAAAACACC ACCCCACCCT GCCCAACATG CCGTGCCGATC GCCCATATCA GAACTAATAA	300
	ATOCTOCOCC ATGTACAATG GTGGCGTTGC AGCAAACGCA AACGCAAAGG CGAATGCGTC	360
30	CAGTIGUAGUA GUTIGUAGGITT CITTURGOGAT GOCCTUCARAT RATINGUGUTA CUAGUARGTU	420
	TATAACTOOT AATGOCAGIA TICOGCCGAC TICATICGAC TAGCICGCAG TATAATATAT	480
35	ATCTAATAIG TACCAATIGT ACTICTITICG ACTICTIATAG AACTITUTICC TCTTICTTGCA	540
	TCACATGTGC AGCACTGCAG CACCGTGCGC CTCGCAATAC TTATGGACCG CGGCAACGGTC	600
40	9900TOGTAT CCASOGTACS CTATGTATCC TGCGGGACCC TTATTOGTGC GCGACACGGG ATAGTGCACA GACTCCACAG AAGTGTTCTC TACAATGCAG AAGA	660
45	(2) INFORMATION FOR SEQ ID NO:1024:	704
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 713 base pairs (B) TYPE: mucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

	(vi) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1627RP
5	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1024:
10	GATCTICCTT GAATTTACTT AGCAGCTOGT TAATTTOCTG CTTCTTCTGC TCTCTTAAGCT
	GGAATCIGIA AAAGTOCIGO TIGGOCITOT TGIOCACCAT GCTGGGAAGC TICTCCTTCC
15	GIGIATOCIT AAGAAGIOGA TIGOGGITCA GAATOCIAOG CCITATOGAG TITAACCATT
	TIGIGITATI COCTACTACA AGIGIGAACO OGICOTOGIO CACAATACTO GATTGAACOT
20	CATCCTGCCC AAGFTGTTCC CGTTGCTCAA ATAACAACAT ATGCTCGTGA ATGTCGCTGC
25	GCAAGIACTC AAGGIUGAGT GOCTTATAGA AGCICIGGAA GGIUGCIATC GAAGGAGACT
23	GGAACGCCCA CTCCACCAAT TCCTTTIGTT TGTGCGCGTA TTTGCGCAGA GCAGCCCAGC
30	AGITOTOCAG AGATOCOTOG TOCACAAACT TOAACAGAGC ACTOTTTOTO OGTGTATACO
	TICIGICCIC COCATOCCCG GIGICICIGA ANTOGGACGT CASCOCACCC ANATOCACCT
35	CGTGCAATGC GAACTOGTOG TGATGTAGCA GCTCTGCCAC ATGCGCCACA GTCTGGTACT
	GCCCCAAAT CCTGCCAAAG CTCTCCTTGA TAGAGTCGAC CTGTGTCAAC AGAGGTAAAT
40	TGACAATAAA CAGGCAATTA GCCTCCGATT CCACCTTCGT CTGATGCTTC CTC
	(2) INFORMATION FOR SEQ ID NO:1025:
	(i) SEQUENCE CHARACTERISTICS:
45	(A) LENGIH: 736 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEINESS: single
50	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1627UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1025:	
5	CATCITICAG ACCCOCCTG GAGAGITTAG ACCAGATIGT TGACCAACCC ATACCAGATG	60
	CTAGACCTGA GTCATACACC CTCCGTCTTG TTGGAGACAC GGAATTGCTA AATTCAAAAA	120
10	TAAAGGAGGA GOCAGATGAA GTGATTGAGG CTATAACGCC AGCTGAACTA CAATGGGAAG	180
	TTGCGGACTT GCTGTATTTC CTCATGGTTA AAATGAGGAG CAATAATGTG ACTTTAAAGG	240
15	AGGTGGAAGC CAACCTAAAC ATGAAGCACA TGAAGATTAC GAGACGGCCT GGAAAGGCGA	300
	AACCAAAGIA CCTACCCCCC CAGGAGTGCC AGAAGAACAA GGAAACTCCT GTAGATATTIG	360
20	CACCATCTCC CATTEACTIC AACGTCGTAT CCTCACATCA TCACCCCCCA TTCAAAACAG	420
25	CAATTACAAG GCCAATTCAG AAAACTACTG ATATATTAGG TCTTGTTGAG CCTATAATAA	480
23	AAAAAGICAT AGAGGAGGGC GACAATGCGT TGACTGAACT AACAGGGAGG TTTGATGGAG	540
30	TAAAGATAGA AACACCAGTA CTAGAGGCTC CTTTTGGCGA CGAGTATTTA AAAGGATTAA	600
	COGNACACOT COGNACOCC ATAGATATTT CONTOCAGAA TOTOCOGNAA TITICATOCOG	660
35	CACAGCTGAG AGACGATATT CTCAAGGTCG AAACGCAACC GCCCGTGGTA TGTACGAGAT	720
	CCCGAGGCCA TAGAGA	736
40	(2) INFORMATION FOR SEQ ID NO:1026:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 707 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAGI628RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1026:	
5	GATCTOCCCC TITAAGCAAC CACATATTAA GCCGCTGACA CACAGACTGT CAGCGCTTAG	60
	AAATACTTOG GTGAGTGTTC AGAAGOCCGA GCOCTCOGAG TTATTCATGA TCACGTGATG	120
10	GGTATTGACC TTGCGATCCA CAGACAGGCG GAAATATGCA TATATGTAAG CCAAGATGCC	180
	GOCAACCAAT TOGTCTAACT GTAATGCATA ACACTGTATT CCGCGAAGCG GCTCTGAGCA	240
15	TGTATGGTAT TOGGOCCTAG ATTGTCAGCC CACGTATATT TOCACGTGAC GCCCTGATGC	300
	TATITACAAC ATAATCACTA TIGACGAGCA AGGATAGIGG TOGCACGITA CGAAAAAGAA	360
20	ACCITICAAAA ATTICCATCC TOCICATCAC CTACACATAT TAACCITAAT CCCCCACCAC	420
	GAATTIGGIC GAAGTICTAT ACTOCCAACG ACGTICOCAG ATTOCTGAGT TCATGGGTTC	480
25	CARAGIATT ARRAGOOG TAGICCCTAR ATTRICOGRA ARROCCARG ACCARGAGIT	540
30	CASCACTICG GOCTCCICIG ATICIACTIT AGAATCAAGT TCATCTTCCT CGTCGCAGGG	600
30	CASCITCCASC ASCASCICIA GITCCTCOSG ACAGIGAATC GASCITOGICG GACASCOSCI	660
35	CCASCICITC TAGCASCASC TOGASCICCT COGGGGAATC GGGCICC	707
55	(2) INFORMATION FOR SEQ ID NO:1027:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 733 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DVA (genamic)	
	(vi) ORIGINAL SOURCE:	
50	(A) OPCANTIGHT DAGICOOD	

(A) ORGANISM: PAG1629RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1027:	
5	GATCTCCCAC ACTAGGCTGG GTCTTACTGT CCATGAATAG CATTCGAAGA ATGGAGGAAT	60
	COGTICTICAA GICAGCOGGG AAAITITICAG GOCAATATAA TOGTITCCCAA GTATTITAGAA	120
10	CITICIOGACT GIOGICAGIA CITOSCOCCI TIAAATOGOC IGITCOCCIT GAAGATATAC	180
	ACCATTCATT CCAGTGTATC GTACCCGAAA AATTAGCAGT AATGGCACTT GCAACATCAT	240
15	CCCGAATCGT GTAACCACTT CCAATAACTG AAACCTTTGT AACACAGGTA AAAATCGGTG	300
	CGCGCGTTCC AAAATTGTCC AATTGTGAGA TTTGTTGATC TTCATTAGGC CTACTGGCCA	360
20	GITCCACTAG TGATCTAACG GGGCTTATTT CAGIGGTTAG AAATTTATCC TTCTCAGTTT	420
	TOGACTITACA AGCAAACTCA GTGAACAAAG GGGGGTATOG ACCAGCAGCT CTTGTGTAAG	480
25	CIGCICAGGI TITCOCTIGI GAAATAACAT GITCITTAGI TICATGIAGG GCTCCAATCC	540
	ATOCOGITAA CTCTTTATAA CTCGTTCCTT CGAAAATTAA AGTACCAGAG TTATTAGAAT	600
30	ATTOTTOCTO AGGIGAAGAA GITAATOGAG AAGAGATAGT CATTOGAAAG CAGTATTTAC	660
as	GIGOCTOTTO TOGATOGICO ATOGCACTOA GIAATAATAC TOCAAATOIG TOOGITTICTT	720
35	CGACTGCAGT TIT	733
40	(2) INFORMATION FOR SEQ ID NO:1028:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 742 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5 <i>0</i>	(ii) MOLECULE TYPE: DNA (genomic)	
	(ví) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1629UP	

(xi)	SEQUENCE	DESCRIPTION:	SEQ	$\mathbf{I}\mathbf{D}$	NO:1028:
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CATCTCCCCT COCTCCTCCC CCTCCA	GCCC TACTOGGCAG	AGCGCTACCC	AATAAACAAC	60
OCCCTAATCG OCCCTOCAGA TAAATT	GCAC AAGCTCTACT	CAACCGATTT	TOCOCCCATC	120
GTCGCCGCCA GCACTTTCGG CTTGAA	CCTC GTCGACAAGC	TTOGACCOCT	GAAAGACCTC	180
ATAATGGCAA AGGTCAGCGG CCCAAA	ITAA TAGICACGIG	TACATAAAGG	TTTTCCTAAT	240
AGCTATACAG CITIGOCOCCG TOCTCA	OCIT GCAGCOGGCA	ACCOGGCGTGC	AGCCATGAGC	300
GICCIACIOS AAACTACCAT TOOCGA	OCTT GTAGTAGACO	TOGACTACAA	GACATGCAGC	360
GCCGAGAGCT ACAACTTOOT CAAACT	CTGC AAAACTCGCT	TCTACCACIG	TCAGTGCATC	420
TACGACCTCC ATCCTGAAGG CTCAGC	ACCC CTCCCCCATC	CACAGGTGGG	CTITGCATTC	480
COCACOGATT TOCCTGTACA CAATAC	CTCG ATCCAAGGCC	TOOGOGACAC	ACGGGCCCTC	540
ACCCCGAAGC TCATTGAAGC CTCCGT	TOOC OCTCAACOCG	CAGAGOGCIT	CGCACAGGTC	600
OCCUTURIES TONASCOCCE CACTOS	COTG CTGCCATCCA	ACATACTOCT	CCCCTTAAT	660
CCCGAACTCG GCCCCACATC AACACA	GIGC GCTTGGCGCA	GCTCATCCAC	CACTOSCTGG	720
CASTICIOCA GCASCICAGO GA				742

(2) INFORMATION FOR SEQ ID NO:1029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 692 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1630RP

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	that opposite projection: Sof ID Millora:	
5	GATCGACTITI CAAACATTAT TATACAGATG GAGGGCATCT CACATCTTGC ACAGCAAGAC	60
	GOCAATOCAA CAGGITOTGI AATGCAGOOT AAGAGGOCAA GGGITGAAGA TGGAGGGTOT	120
10	AGTGATOGAG AAGTACGAGG AGAGATAAAG COCAAGTATG GTATTOOCOC GCAGTTGATG	180
	GCCAAGATGG GATATAAGGA GOGCAGCOGT CTAGGGAAAG AAGGTACGGG ACGCACGACG	240
15	CCCATATTGG TATACCACCE GCCCCACCCC ATGCCCCTTG CACCCAACCT CTCCATTTCC	300
	TCTCACTCAG ACCAGAGTGA GGTGCAGCTT GTGACTCCCC AGGCAGTGAA GTTTGAATCG	360
20	AAAGGTGTGG AGACTGACAC AAGCAGAATA GCAGACAAGA TAGCAAAGCT GGAGATCGCA	420
	GGAGTGCAAG TCCCCCCAGA AGTGATGAGT TTGCGTTCTG GGACAAAGAC GCTGGGTTAC	480
25	CAACGGGCIG CAGCGATGGA AAGGGTGCTC TCGGAACTGC TGCAGGTGGG TGAGCAACTT	540
	GCGACCCTAC AACTACGCGA AGATCAGCTG CAGCAAGGGC TAGATGCGGC CAITICAGAGT	600
30	AGTGACCTGT TGAACAAGTT CTCAACGCGC TGCAACAGCC GACTGCGCCTG CCGGAGCCGG	660
a.e.	TAGCGGCATA TIGGCCTTGG AGGACCCAGA AA	692
35	(2) INFORMATION FOR SEQ ID NO:1030:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 712 base pairs	
-	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1630UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1030:

	CHICATORICA DETACACO MOGRADAM CICADARCO GEOGRAPICA	60
5	TERRESCRIP CONCERNED CONCERNED CONCERNED CONCERNED CARCONICON	120
	ACCOTATOOT CCCCGACAAA TGGCGAGGGG TAGATGATGC CCTCCTCCCC CTCCCGCCGTA	180
10	COGCOGCICT COGGCGTCTC CGCCTCCTCT GTCCCCCCTC GCCCCCCTCCC GTCCCCCACAC	240
	AAACGGTGCC CGGCCGGCAC CCCAACGCGG AGGCCTTCGG CGGCGGCGGC	300
15	COOCTICCOCC CTCCCCCAAG GCCCTTGCCC TGACCCAGTC CTGTAGGTGG CTGGTGGTCA	360
	TOGAAGGGCG TOCAAGCAAT TOGTGTACGA TGATCTATOC CAGCOCCAGC CTTOGTCACC	420
20	ACCOCCOCA GCTGCGCAG CITGCGTTTG GTCTCGTCCA TATCGTCGTC TCCGTCTCTG	480
	TAGGCATCAT ACATCTCCCG CTATCTTTCT CTTGCGCCTG CACCGGTACC GTGCATTGCA	540
25	AACOCTOCTC CTGCCCCAGG GCAGTTCTAT AACGTTGCCA GTGAAAATGG TGCAGTACGG	600
	AACAGTAGCT CATOGCGCAC CAGGCGAACA CATAGGCAAC AGCTTGGGTG TAGGGGGCTG	660
3 <i>0</i>	CGGGCCCGAC CACGATACTC ATGITTACATA GACTICACATG ATCACGCAGC AC	712
	(2) INFORMATION FOR SEQ ID NO:1031:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 729 base pairs	
	(B) TYPE: mucleic acid	
40	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1631RP	
	(A) ORDANISM: PAGIOSIRP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1031:	
55	GATCTAATIT ATTTACATTA ATTAATAATT AATAATATT AATAATATTC AATAATTTAT	60

	ALATTIAAT ALATTAATAAA TACTTAATT ACATAAATAC TTTAATTAGA	120
5	CAGTTAGGGT TCACCCCCCT AATGCTTATC AGCATTATGA GGTACCACTC TAATTAAAGG	180
	TAAATATATA TATTIAATAA TAAAAGGATA TAGITIAATT GGIAAAACTA TIGACTICAA	240
10	ATCAATCATT AAGAGPICAA ATCTTTTTAT CCTTGTTATA TITTAATAAT ATAAATTAAT	300
	AAATAATAAA TATGATAAAT CATAATATTA AAGATATTGA TTAATATTTT TAATTAAT	360
15	AATAATAIGC AATTAGIATT AGCAGCTAAA TATATTGGIG CAGGTATTIC AACAATTGGI	420
	TTATTAGGAG CAGGTATTGG TATTGCTATT GIATTTGCAG CTTTAATTCA AGGTGTATCA	480
20	AGAAATCCAT CAATGAAAGA TACTTTATTC CAATTTGCTA TTTTAGGTTC GCTATTAGTG	540
	AASCTACAGG TETATICIGT TEAATGATTT CITTCTTATT ATTATATGGT GITTAATTIT	600
25	ATTAAATTAT ATAATAATTA ATATTCAAAA TAAGTTATAT TAGCTTAATT GGTAGAGCAT	660
	CCGITTIGTA ATCGAAAAGG TIAGGAGITC AAATCICITA TGIAACAATT TAATTAAAIT	720
30	AAATAAAGA	729
	(2) INFORMATION FOR SEQ ID NO:1032:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 716 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(b) lorologi: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1631UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1032:	
55	CATCTTAAAA TAAGATAGAA TGGTAATAAA TATCATTCAG GTACAATAGA TGCTGGTGTT	60

	ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
5	ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGTTA CTAAATCTTT AAAAATAAAA	180
	TAACCATOCA TIGGIAATCT ATCTAAATTA CCIGTAATAC CIAATGCATT TGAIGAACCA	240
10	TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGTACTAAA	300
	TAATGAAATA GAAAGAATCT TATAATAGTA CCATTACTAA CACTAAATGA TOCTCATAAT	360
15	CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	420
	CCACCICAAT GIGACATITIG TOCATATACT AAACAATAAC CTAAGAAAGC TOCTOCTATA	480
20	GTTAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TYTATAAGAA	540
	CCATAATATA AACCTTTACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA	600
25	TTAAGATGCA TATATCIAAT TAATCAACCT AGITGTACAT CICICATAAT ATGITCIACT	660
	GATGAGAAAG CIAATTCAAT ATTAGATGAA TAATGCATAG CTAAAAAAAT ACCAGT	716
30	(2) INFORMATION FOR SEQ ID NO:1033:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 658 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDECNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1632RP	
45	(25) CALCARLLAIT. FROTUSZKY	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1033:	
	GATCTTCGCG CCGTTGCCGC CCAAAACCCCG CAGCTCCCCAT ATACCCGTGT TCAGGTTGAA	60
55	GCTGATGCTA GCGTGCTGCC GCGACACCAC TTTCGCAGGC CCCAGGTGGA TGTGTACTGA	120

	considered comparately recorded acteditate attrictues constituted	180
5	CCAGICICAT CCCGATATCT TOOCGIACOC CIGIACTICC GTIOCCGIGT TCTTGICGIT	240
	CGAATATACT TOCGACACTG TOGTOOCCTC CTTCGGGGCA TOCAGCACCG AAATCACGGC	300
10	ATTICATICACE TECTISTICIOS GITAGIACTE GETETOGIOS COCCOGNETE GETECTACAT	360
	ACCIDETEGT GETECTGAGA COCAAATOOG TAATTCATET CGTOGOCTCA ATTTCOCTCE	420
15	TOCACTOSCT GOCCCAGGGT AACGTOGGAC TTOCGTTGCT GTGCAAGGGG TGGTOGCTCA	480
	GCGTACCTCG GIACAGCIGA TCTCCGGICTT AGTATCAACA AACCAAAAAT AAAAATAATA	540
20	ACAATAAGCT TITICACIGIG TGIGAACGTC CCAGAAACTG ATTICCAACGC TCCAACACGG	600
	CACTICITEA AGCAACCICA COCACOCTIC TEAATGACAG ATCACOCTCA CTAAACOG	658
25	(2) INFORMATION FOR SEQ ID NO:1034:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 690 base pairs	
30	(B) TYPE: mucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
	(=) Posteri. Initia	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1632UP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1034:	
	GATCCAGACT GTGATATACC TGTATAAGAA GGTPTGGAAA CCTTAGTAAA TACCCAACTT	60
50	TTTTAATTCG AACCTTGTAC ACGITTTATA CTCAATTGTA GCTTTGAGTT GCAAATACCC	120
	GAGGCATAAA ATCAAAGOGT ACTTAAAAAC AATCACTACA TACAGICCIC CACACGCIGC	180
55	CAGAGICGAA TAACAIGAAG AATAAATATT AAGGACAGTA AIGCIATAAA TACAIGIGCT	240

	TCAAATAAAT ATATGCTTGC TAAGGGTTTT CAAATTCGGT TTGCGGCAAA GAGTACGCAA	300
5	TANGTOGATO TTOOGAAAGT GATGGGGGGA GATAACGACC AAACAAGTGA GTTTCCACGT	360
	TACCIATATC TICCICIOS ACAAAACTOC CACIGIIGAC CATIGITGIG CIAGGIGITT	420
10	GATGIATOGA TOGAGIATCA GCACGICCOG TAGAGGAAGT GOGAATTAGT GAAACTAACG	480
	TCCCCCCAGAA ACTOGATCCC ACACGATTGT TIGGTAGTGT GGGGGGGCGTG TTAGGATTTT	540
15	TAATGITGGT TACTGGGGTG CCTGATGGCA ACGATGGGCC AGAAAAGTAT ACTTGCTCCT	600
	GIGCITICAA AGATOGGICA ACAGCCCAAT TGTGAAAGAA ACTGGCATTA CTAGTCTCAG	660
20	GGATGCTAAT AAGCTCTTGG ACAGAGTTGT	690
	(2) INFORMATION FOR SEQ ID NO:1035:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 749 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1633RP	
	(-,	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1035:	
45	GATCAATTAA TAAATGGITT AACTAATAAA GTTAATAATA AATGTATTAA TIATATAAAA	60
	CTACCICATT TTATICAATC AAATAATATT TTCTTAATCA ATACTACTAA ATCATCATCT	120
50	ATTGAGTTA TATTAAATTC ACCACCTOTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
	TCITAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGIGGATAT AGITTAATIG	240
55	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300

	AICAITAATA TAADAACTOT TTAATTAGAG TOGTACCACA AGAATOCTGA AAGCATTAGG	360
5	GGTGTGTACC TTACCTCTCT AATTAAAGIT ATAAAATTAT CITAACTAAT AAAAATAATT	420
	AATAAAAA ATAAATAATT AAATAATTT AAAAATGITTA AAAAAAAAA TAAATAATAT	480
10	GITATATTA AATAGATCAA AATTTCAACA ATTTCCATTT CATTTAGTAC TACCATCACC	540
	ATGACCAATT GITACATCAT TTAGTITATT AGGTPTACTA TTAACTTTAG CTPTTACTAT	600
15	ACATGGIATT ATTGGIAATA TTTATCCTTT ATTATTATCT TTATTAGIAG TTTTATTACT	660
	AATAACTTA TGATTIAGAG ATATOGTAGC TGAACTTACT TATTTAGGIG ATCATACTTT	720
20	AGCTGTAAGA AAAGGTATAA CTTAAGGTT	749
	(2) INFORMATION FOR SEQ ID NO:1036:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 732 base pairs	
30	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
<i>3</i> 5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1633UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1036:	
45	CATCITAATT TAAAATITTA ATTAACTATT TATAATTTAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
50	AATAGAAAAC CATAAGTTAA TIGATICATA AAGAAAAATG GAATTATITG TOOCATCITA	180
	ATTITITATIA TITAATIGAT TATTATCIAT TIAACATAAA ACATTITAAA ATGITATAAA	240
55	ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TITTAATTTAA TTTTAATATT	300

	AAATATACCA TITTITATTAA TAAATAGATT AITAAGTITA TIAATATTAA GIGATATATA	360
5	ATTIAATTA TATAAATTAT TTAATTIACT TCATTGATAT ATATAATTAT TAAATGIACC	420
	TTTCATAATA TITATTTTTA TTAGTCTAGT AATATTICTA TTTAATAGTC TACCCITTAA	480
10	TTOGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	540
	TAATAATTA TTATCTAAAG TATATAAATT AATTAAATCT TTTTTATTAT TATTTAAATT	600
15	ATTATTAATT AGTAAATTAT ATTTATTTAT TITATTAACA TAATTITTTG ATAATAATAT	660
	ATCATTATTA AATOGITAAT TTATTAATAA TTATCTTTAA TGATTTTAAT GATAAACCAT	720
20	TATTATTATA GA	732
	(2) INFORMATION FOR SEQ ID NO:1037:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 702 base pairs	
	(B) TYPE: nucleic acid	
30	(C) STRANDETNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1634RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1037:	
45	CATCCATCTG CGGTTTGTGC GACGTCCTGT GAAACTCTAC CAGGCGAATA GAACTCTGAT	60
	AGACGACTOG CAGGTOTCTG TTGAGTOGCA ATAACGGCAT TTGCATCATC TATATOGGCA	120
50	TICCIGGIAG TATCIATOCT TAGACTOCAT AGGGACCCAT GCTTTACAAG TICAGGTTIC	180
	OCTIOCOGAG CCACGACATC CTTTTCTCGA TITAGGAATG ACAAAATTGA GGAGTTCCTC	240
55	CTATECTTET GITCAAACTC ACCAGCAATE CTEGCTCGTT TATTEGTACT CECAGATACA	300

	TICCTIGAAT GICCATAGAT ACTOGAAGAC GGCCTTCCAG TGGGAGCTGG AACGGCCAGA	360
5	CTGTCTTGTG CACCTAGCCC TTCGTAATCG TTTCGAGAGG AAAGCATGGA AATTCGATTG	420
	AACAACTOCA CAAACGAGOC ACCOGATTIT GTOTTOTTAT GTOTOSCTOT TATACTOTOT	480
10	TCCGGAATGG CCCTTTCAAA AGTACGCTGC ATCGGAGATA TGCCAGGATT ACTGTAAGGA	540
	TITICCAAGGI CIGGOCCATC AGGCTGITCG TCCACAGCAG GCTGCATAAA TACTGTGGGA	600
15	TAGATIGCTT TCTCCAGGAA GTGTAAGAAG CTGGTGAGTT TAGGGTTTGT GGGCCGTGTT	660
	CGTAAATGGT AATGTGCTGA TTCCTGGCTT GATTCTGCAA AA	702
20	(2) INFORMATION FOR SEQ ID NO:1038:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 736 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1634UP	
40	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:1038:	
	GATCACAGOG TOGOCCAAGOC CAGCATTGTG TCTTAAGTTAC ATGTAGAGGT OGAACAGCAC	60
45	GAGGGAATGC TITTICCCIAC GGCGGAATIC GAGACCTICA GACTGACACC GCAGATTTIC	120
	TGTGCGGCTC ACCGACCCTT AAATAGCTAC AGCAACACAG CTGCGCCGGT GTACACTGAT	180
50	AGCAAAGATG AACCOGTCTA TCCATTCGTC GGTGACTGCG ATGGCCTCGG ACGACGCCAG	240
	CAGTOTTOGG CATGAGOGGT CGAOGTACTC GGCGGAGTCA GAGGAAACGC TOGTCAACTC	300
55	GTATGGGCCC TACAGCACCA COGGAATCGT GATGACATCT GTGATGATGA ACAAGGCCCA	360

	OCOCAAGOOC CAAGTGTCCG AGCAGTGGAT GCGGCTCTTC CTGGACAGCA CGCCTGTCGA	420
5	OCACGTODOG GTOCTOCAGO GCOGGATGTO GGTCACOGGG CGCTGCCTGG ACACGTTGCA	480
	OCCUPATION CARAGORITOS ACCIGATACOS CORGATOGIO COSCOCIOS CONTETIONA	540
10	ACACOCATGE AACCTGCAGT GCTACCACGG CAACGAGGGG GACTTTCCGC TGCTGCACGT	600
	OCCURATIONAL GIVANCADOC TONOCACACT GOCCADOCTIG CTIGGTOGNOC ACOGOGTIGTO	660
15	COGNITACAGE ACCOCCATOS ACCAACTEAC CACOGNOCTT CAGNACETECA ACCAACETECT	720
	OCAGOGGICG COCGIC	736
20	(2) INFORMATION FOR SEQ ID NO:1039:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 737 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: 1635RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1039;	
	CATICCTAGGG TGGTTCATGG CACTGAGCGG GACCGTGTTC TTGGACCGGT CGAACCGCAG	60
45	CAACAGICIG AAGICGCIGA ACGCGICGCT GGAGCGGCTG AAGCCCAATC GGCAGGCGGC	120
	GTGGATTTTC CCAGAGGGCA CGCGGTCGTTA CACAACGGAG ATGCAGCTGC TGCCATTCAA	180
50	GAAGGGGGG TTCCACCTGG CGCAACAGGC GCAGATTCCG GTGATTCCGG TTGTGATGTG	240
	CANCACGAGC ACGGIGITCA ACCCGCGGCT GGGCATCTTT AACCGCGGCA CGATCACGGC	300
55	GARACTICCTIC CACCCCATCC ACACCCCTAA CATCACCAAG CATGACCTICG ACAACCTTGT	360

	GAGCGACGIG CAGGCCAAAA IGCAGGGGA GITICGAGGGG CITIGGCIACG CGCCIGCGAT	420
5	COTTOGAÇÃOS ACCOTACIOS ACCACIOCOCT COCOCOCAS TITUOTOGACT OCAACGAAGA	480
	CATCACGGAG GTAACGCCCC TCTTGAAGTA ACCTTGGTTG GTATCATATA AACGTTGCGA	540
10	CGAGTTATGT ACATATAGCG CTGCTAAGTA GGCATTCAGT CQCACGAACT CATACCTGCG	600
	TOAGCTOTAC GOOGGGCCCA TETEGGGCCAG ATACTTETOG ACCTOCCCAG COGACCOCAG	660
15	CCACATOGAG GACTIGICGI GCATGIGCIC GGCAGIAAGG TOCAGAAAIG CGCTGGCGC	720
	GETCGITCAC GECCITG	737
20	(2) INFORMATION FOR SEQ ID NO: 1040:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 686 base pairs (8) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1635UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1040:	
	CATCOCACTG ACOGTGAATA GOCCACOTTA GCATGOGOCG CTGAGOGOCG TGGOGAGOGA	60
4 5	TAGCAGOGGT COGTCOGAGG CTCTGGTGGC CAGGACAAGG ATCCACTGGC CCAGCACGC	120
	CASTAGGAGG ACTIGOCCACT GGACTIGACAT OGTOGACACA COGTTIGUGGA TIGOAGAGGTO	180
50	ANTINICAAG COOGACAGGA AGOGOGAGCA CGTOGAGGCA ATCOCAAATT CTGGCAGCAC	240
	CGACGCCTGG CCCAACAGGC TCGACAGCCA GCCCATGTTG GTGACGAACA TCTCCATGGC	300
<i>55</i>	GCCCAGCGAC AATAGCAACA CAAGGGCCAT GAAGTACGCC GCTGGGTCGT GGAAGAAGIT	360

	CCCCACCCCC CCCCCCATGT CCTCCCCCAG CASCCCCTCC GTGCCCCTCT GCATGCCCCC	420
5	GAAGGICAGT GITIOCOCCCT TGACCTTGAG CATAGTGAGG ATOCTOGTOG CAAACCACAT	480
	GCAGAAGCIG AICAGCGTAT ATGCGACAGC AAGAGTCCTG AATACACGAG AAAGGTCAAG	540
10	GTACGGCAGG CCATTTCGAA ACCATGGTAT CTTCAGCAGC TGCGACCCTA GCACAGACGC	600
	CATCCCCTAA AACGIGGCCG GCAGACTTAT CGAGCACAAC TIGCTCGCCG GGIACAGITT	660
15	TCATGOOGIG AACAGCGCAC TCAAGT	686
	(2) INFORMATION FOR SEQ ID NO:1041:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1636RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1041:	
40	GATCTTCTTC TGCTCGATGG ACGAGCCAGT TGTATCTTGG ACTCTACCGA TAACCCACAC	60
	CITTICCTIC AGCCACAGGA ACTICOCATC GGITGOGITA TICOGGIATA GATATAGCOC	120
45	TACGANCOCT ACCACAAACG TTAGGCTGOC GATTATAATT GACAGAATTT TOCAATGTGA	180
	GATAGCTGGG TTCTTTATCA GCAGGATCAA GTAGGAAAGG ACGCCCATTG GTATGGATAC	240
50	ACTICACCGTC GOGATAACAA AAATCGGGGG GGTCGCTGCC TTTTCATTCT CTGTTAAGAA	300
	CATCAGCATT GIGITGITCA ATGCAGGAAT GATAATAGCC TCCGTGAAAC CTAAGCAGAG	360
55	ACGAAGAACA TATACACCTT TGTAATCCCT CATTGCACAT TGTACCATCA TAATGATGCA	420

	CCATATOGIC ACCACCACCA TAACAACGIT CTTCAAACCA AACTTCTGGA TAAACAGCAA	480
5	GITGATCIGI CCOGTAATAT AGOCAACGIA GAATAAGGIA TICACATIGI TGIAACGATT	540
	CAAGGACATG TTTACATCTT CAAAAAATCC TAACAGAGIG CTGTAGGACA ATTGCGCCTT	600
10	GICIATGIAG GIGAIGAAAT TAATOCTOOC CGICAGICCC ACGAIGIACC ACATAACCIT	660
	TOGTOCAAGO TYCTTTTOCT COOCTTCTGT GATAGGAGGG ACATCCTTGT CTTGCTTCAA	720
15	(2) INFORMATION FOR SEQ ID NO:1042:	
20	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 677 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1636UP	
35	(>d) SEQUENCE DESCRIPTION: SEQ ID NO:1042:	
	GATICOGCAAG ATGACOGAGG GIAAGGGCCA CCTGCTTTCG CACCACCGCT TAGTTTCCTT	60
40	TOGAGGIOCA GGIOGICAAC ATOCAGITIGO AGTOCCACAC TCATTIGGOCA TAGAAACOGI	120
	CCTCATGCAC AGGIACTCAG CAAITTITATIC TGCGTATGGA ATGCTTTTGG CGGATGCGGT	180
45	AAAAGAGGAG CAAGTGCCAT GCTCCATTIT CTTGCAAGAT ACATCTTCTA AAGACCAGCT	240
50	AAATGAAATA TICCACCAAT IGATTACCAG TACCICAATT AGCCITCTIA AGCAGGGAIT	300
	OCCOSACIGNT COSCUTIGNAT TOGRIGAGATA COTIGNACUTA COTTATIGNOG GIACTIGNAAC	360
55	AAGTOTTATG GITCTACAAG AAGGAGACTO GTGGGATTTT GTAGAAAGGT TOACAAAACT	420

	CCACAAGOGT GAGITIGGCT TIGITITICGC OGAGAAGAGG ATTITIAGTOG ATGATGICCG	480
5	TUTOCUTOCT CTAAGTAAGT CTATOCTOOG GAACAGCAGC CTUTTGATCA GCAGTTATCC	540
	CAGGICACIC GITCIACAGC TGACCCTTCT AAGGATGCAA AGTTCITTAA GGACGTGIAT	600
10	TTCGTCGATG GGTTTATTAA GACCACCTAT TTACAGGTTA GATAGTTTAC COGTAGGTAC	660
	CTGTATTGAA GGACCTG	67 7
15	(2) INFORMATION FOR SEQ ID NO:1043:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 726 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEUNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1637RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1043:	
00		
	GATCTOCTCA TACTGAGCOG CCAACTOGTC GTACTCCGTA TOCAAAACAT CTGTOGTTTC	60
40	CTOGRAGTOC GCCACCITGA GCGATATCTC ATTAAACTTG GTAACCAGCT CTCCCAACTG	120
	ATGATTGACT GCACTGGTTT COGTCAGCAG GTCCTCCAGT TCGCCAGTTC TGGTGTCCAC	180
45	TICCGCCACG TATCCGCTGT ACAATGTATA CTCGTCGTTC GCAGACCCCA GAGCAGAAGC	240
	TOSCOCCAC TOTOCCCCA GCASCTCAAT TACCTCAGGT TCAATCTCTG TTTCAACCGT	300
50	TOCCAACAGA GTGTCTACTT TTTGGCGTAA CGAACTATCC CCAAAAAAGCG GAGGCAGCTC	360
	ATCGTGAGAG GAGGCACCGG GATTTGCCGC TACATCCTGT ATGACTGAGT TCTTCCCGCT	420
55	CCTAGGCATG GTGCAGTTGC TGCCTCAACG GCTTTCTTCC TGGTGCAGGT CTGCAGTGGT	480

	TOGTOCTTAT GOCCAAGCAG AATACCATGT TGAGCCGCG AAATCTCATC ACGTGATCAT	540
5	CATCTTGCAA CGGCTCGGAG GACGCTGATG CACTGTTCCA TAGGCTTAGG GCGCAATTAT	600
	ACOCTACCTA GITATATICA TAATATOTAC ATGATOCCIT COCCACGACA GOOCACTCAG	660
10	TOCTOCOCCE COSCOCCCC CTCCCGCAAG CTCTTGTCTC AACTTGCGCCC TTCTCGGCCT	720
	CCACGT	726
15	(2) INFORMATION FOR SEQ ID NO:1044:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 683 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	,_,	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1637UP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1044:	
	CATCTICCCC TCCTTCTTGT CCACCTGTAG GTCCCCATGA COGTACCCCT COCTCAGGTA	60
40	CTCCAGCCGC ACCTCCCCGC TCTCCATGCA CGCCTCCAGG ATCGAAGGCG CCCGCACAGC	120
	CTCGGAGGGG AGGGGGGGT GCAGGAGGGG CATCTGCTGT CGCTGCTGGT GCATCTGCAG	180
45	COCCOCAGOG CTCCGCCTCCA GCCCCGGGTC GAAGTACTTC ACATTGGTCA GCCCGGACTT	240
	GTACAGATTC AGGATGCAGC OCTTGAGCTG COCACGGTGC AACGGGTAGG CAGTGGCGAC	300
50	ATACTOGTAC COCCIOGICC CCCCTCCCGT GAACTGCGGC CCCTCCCGATC CGATCGAAGA	360
	CAGTGAGGCT GTTGGCTGGT GGCTGTATGG CCCCTGGGGC GCGGGGGCTG GGCCCTGGGGC	420
55	CTTGTTCACC CACCCGAGCC GAAACACAGT CCCGTCGTAC GTCTCCCCGT TCAGCCCGCC	480

	TCCACGICGC ACCGGCGAGC CCGCCGGCTG CGAGCAGGGC GACACCTGCT CCTCGCAGCG	540
5	COCACCCOCC TICATGICCT CACATGICAG CGICCOCTIG TGCCCTTGCC CCGICGSCAC	600
	CTGTAACTOC ATCOCCGTCT GTGCCTCCTG CTGCTGCTGC TGCGTGTGCT GTTGCGGTTT	660
10	OCCIGITOCC CITICITIGIT GIA	683
	(2) INFORMATION FOR SEQ ID NO:1045:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 665 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1638RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1045:	
35	GATCCTGTCG CTGGAAATGT COCCGACCAG AACAGACAAC CGTCCCGGGCC GGGCCGATCT	60
	GCCGGAACCT CTCCGAAGGA GACCAAGAAG GAAATTGTAA AGCTGCAGCC AGCCCCGATT	120
40	CCACAGAACT CTCCCTTGGAA ACCOGTTGCAG ATTGGGGACGG GGGCCGACGGAG	180
	GACGGCCCCT GGCCTTCTGC GCACGAGGTT GCGACAAAGC TTGCTGACGA CGGCAGCGGG	240
45	CGGGGGGCCT CGCAACCGAT GGTGACGACC GGGAAGGACA AGTGGGTGCC AATGAAGCCG	300
	GCCATGCTTG TGCCCCGGCA GGGCTTGCGC AAGATGCAAC GCAAGAAGAA AAACGGGCAG	360
50	GCGGTCAACG GCGGTGCCGC GAAGCGCAAG ACCGGAAACA AGGCACCCCC CAGCCAGC	420
	AAGAGAGCTC CAGACTCCCA CAGGAAGGGG CATGACGAGG CGAGGGCCGC GAGGGCCACG	480
55	CCATCTECAC CEGAGGAGCA CETTEGAACAG CECGAGCTCG ECGAGCAGCA ECAEGTCCCC	540

	GREECICAS ARCHEGIGO GENERICOS REALASCAIA IGROCAÇÃO GENERICOCAS	600
5	CCCAGAAGAC GCTTCTACGG CGGCAGGCAG CAGCACTCCG CTGACGGACA CAAGCCAGTT	660
	TGIGT	665
10	(2) INFORMATION FOR SEQ ID NO:1046:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 765 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1638UP	
25	(A) CANIGNI PARIOSOF	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1046:	
	GATCTGAGAA CTACTGTGTG TCGGCTAGCG CAAACTTATC AGAATTCCAT CAACTCACCG	60
35	AACCATAGCA CATCTACGIC ACCTCCCCCT ACCGCTACAG ATACCGGGAA TGATCAATTT	120
	TIGOGIGITO ATOCTIGIAAC CATATOGCAT GATGACAAGT ACCTAATATIG CATGAGCAAT	180
40	CACACGUACA TUCATGUCIA OGACATGUCA GAATUATCOC CUGATUGUCA ACOCTOOCAC	240
	GAAATTAGGA CTCCTAGACT ATCTAGACTT AATATTGGGA AGCAGATGAT GTCCATGAGC	300
45	GGGCCAGFIG GACCCGAIGA TICGCTITTA CTAATCAGIG TACAGCCACA CGAGCTICAG	360
	CTATGOGATT TCAAAAGOCA GATTATGGTC CAAAGATATG TAGGACAGCG GCAGGTGGCA	420
50	TACATOATOC GITOGIOCITI TOOGIATOOG CACAACCIAG TTOCIOCAGG TTOCIOCAGC	480
	GGGAAGATAT ACATTTGGGA TAGATATTAT GGIAATATTA TIGGCGTTCT ATCTGGGCAT	540
55	AACATGGAGA GACCGGACGA CTCCAGAAAT AAAAACTTCC CAATGACCAA AGTTTGCAAT	600

	PERSONAL CONTINUES CINTITOCOL CIGARANDA TEARRICIG	660
5	GIGAAGATAT GGAAGGITGA CCCTAATTGA TGAATCCTAT AGCATGACGT TATTTGTCTA	720
	TAGAACTICG AGAAATCCTG CCCATCIGIT GITTCCTAAA TIGTA	765
10	(2) INFORMATION FOR SEQ ID NO:1047:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 658 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1639RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1047:	
	GATICCATCIG ACTATIGITT CACGOCATIC GOGGACCAAC TGTGCAGTCA GOCCCAGGAA	60
35	COGGGGGAGAAA TAAGCCTTGA ACGAGCGCTG GTOGATATTA CAGTTGTCGC CACCTTGACA	120
	TOCTOCCTOG TACAGGGTGT CGTTGCTGAG GAAGATTCTG GCGCTGTCCA AGAAACGCAG	180
40	TETTCOCTOG TECCACAGCT CETCCTOGET ATGETTGTAG ATGAAGGCAC AGCCTGCCAT	240
	GATCAGCCCA TEGTTETAAG TCCACTECAG CITATTTAAG TTEGTACAGT TGTCGTTGAT	30 0
45	GICTGIACCC TCGTAGACGA CGTGCCAGTT TCGCTGCACA ATCGAGATCA GCCCAACGCC	360
	ATACATOCAG TOGTAAACCC GITCOGCCCA CTCTAAGTAT GIGGCATTCC CGGTGTAACG	420
50	CEPTAATOGT GOOGCCATGT GCAACAGCGC ACCGTTGGAA ACGGAGTTTT TGTAGTGGTA	480
	CCCGTCGTTC CAGCGGAAAA TCTGCCATCT GAGCCGGCCG TTGCACGTCT CCATATOCCA	540
55	GOGCAGGGC ATGGTATTAA ACACCGCCTG CGCCAGGGCC AGCCAITIGGG GCTGGTCCGC	600

	GGGGGGTTC GGGAAGTTGC GCTCCCCGGC AGCATCACC GCCATCCCCC AGAAAAAA	658
5	(2) INFORMATION FOR SEQ ID NO:1048:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 730 base pairs	
10	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1639UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1048:	
	GATOCAGOGG GTGAGGGACA COGTGCACAT AACGACTGCG GACGGTGCCT GCTATGTTTC	60
<i>30</i>	CAAGTGCGCG ATTGTCACCG TCCCCCCAAAG CGTGCTGCAG CTGTCTCTCA AACCACAGCG	120
	GETGCCCGGG CGCATTGAGT TTCCCCCCCC CCTCAACCAC AACATCACGT CTGCGTTTGA	180
35	GOGAGOTOAC TACOCCTOGO TGGGCAAGAT CTTCTTTGAG TTTGACAAGT GCACCTGGGA	240
	CACGCAGOOC COCCOGGTTG CTATOGCAGC CAAAGTTCOC GACGACTTTA GTGOOCAGGT	300
40	CCCTAAGGCC CAAGATTTGC AGGAGCTGCT GCGATCCGCC AGTGCTCAGA CTGAGGTGAA	360
	GCTGGGACAA GACTGCTTTG ACTTTCCACA AGAGTTTCAG AACATGGTTG CGCTGGCAGG	420
45	GATACCGACA CTTATTGCGT TCACGCAGAC ACCTCTTACT GAGCACGTCG AGCGCTTATC	480
	AAAGCAAGAG ATTGTGGACT ACTTCAAACC COCAATTGTT GTTGCACTAC GTGCACTGGG	540
50	GTCCAAGGAG GAGTGCCTCT TCGACCTCGG AAACACGCAA CCGCAAGACG ATAGTCATCC	600
	ASSCCCAATC CTAAAGAACG TGATCTTCAA TCCGTGGTCA CAGGATACGT ATTCTCGTGG	660
55	CTCATACACC GETAGTCACG TGCACGACGA CCAGCTGCCC TTGAACGTGG CCCTCAACAA	720

	CGGCCAAGAT	730
5	(2) INFORMATION FOR SEQ ID NO:1049:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 702 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1640RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1049:	
20	GATCAAGCCG AGCACGCTGA CCTTGGCTCC CCGACGCAAC ATCGGGTTGA CGGGCTCCCC	60
30	COCCUTIOCOSC TOCTOCACOSC CATOSCOCAS CITIOSCACTIC OCCOCOSCOSCO	120
	GAGGOGGGC ATGTOCATGA AGACCGGGGAT GTACGAGCCC TCCGTGATGG TGTATATAGT	180
35	GITACAGCAG AGCATCAAGC AGTACAGCAC CGACATCAAA ATGAGCOCGC CGTAGGTCTT	240
	OCTACCCTOG CTGACAAACG GCGTGGCAAG TGCGCCGTTAC ATTACAATCG ACAGCGTCAT	300
40	GAGCCACTIG COGTAGTITIG AAAAGTCCCC CAAACCCATG AGCACAATCG CAATGAGGCC	360
	CTOGATOGAC GTGTACAACG CCCGCATATA AAGCACATAT GCCGTGAACT GCACGTCCCT	420
45	TCCGCCCACG TAGATGINGC AGTCATCGCC GCGCGGGGCCG CAGTGCGCCG CGGGGTGCCCC	480
	CTTGGGGTGC CCCAGCTCGT GTGGGGTGGT CTGTAACGAC GCAGGCACAA AAGAACGCAT	540
50	CATICACITIAG GTCGGCCCGG TCGAAAAGCA CACAAGGAGC CATGCAGGAA ATACCCACCG	600
	GCCCCGCCAC CGCCCCACCA CTCCTCCTCC GCCCCACTAC CGCCCACTAG CGCCTCCTGC	660
55	TOSTOCADOS TOACIGAÇÃO CIGOATGICA GOGOCOCTIGO TI	702

	(2) INFORMATION FOR SEQ ID NO:1050:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 696 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1640UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1050:	
25	GATICAACGAG CTGGGGGAGC TGCAGCTGGA CGATGCGGAG GAAGGGCTGG AAGAGGCCGG	60
25	TOGTOCOCAG GAGOCOCOG COCTGTOCOC OCAATTOCAC OGTGACGACG ACCTGAAGGA	120
30	GUACCACUTE CAGCACUACE ACCAGGAGA TOCOSCOCCE CETOCAGACE TCACCAUTUT	180
	CCCCCCCCCC TCCCCCCCCCC CCCCCTTCCA CCACCCCTCAC CACCCCCACC ACCCCTTACCT	240
35	CACCITICOCA ACOCTACAGE ACCACOAGGA CCACOGGGGG CACCIGCAGE IGIACCOGAC	300
	AGACAACCTG GTGCTGGCAA GGCGGACGGA AGACGACATT TGGTACCTGG ACGTGTACGT	360
40	CTACCACAC COCCOCCCC TOCACCACA COCCOCCC CACCACCCC CCCACCCCCA	420
	OCACCOCCAC GIGGOGGGGG GGCIGATACG GGAGGGGICG TIGIACGIGC ACCACGACCI	480
45	CATCITICCOC CCATTCCCCC TGTCCCTCCA GTCGGTCAAC TACCCGCCCG GGTCGAACTC	540
	TEACGCGCG GCAAACTTTG CGGCGGTCGG CACCTTCCAC CCCACGATCG AGCTGTCGAA	600
50	CCLECACIEL GLECACOSCO CCLCCOCCAC VLCVLCCLCC CCCACOCCCC CCACLCLCCCC	6 60
	ACCECCETCCA ACRAGETCCAA CAACAACAAC AACCECC	696
55	(2) INFORMATION FOR SEQ ID NO:1051:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 725 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1641RP	
,,		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1051:	
20	CATCOCITAG CEACTICTIC CACCOCTICGA CGAGGCCATT GAGCTCTTAC GAACTIGCACA	60
25	AACCTACTOG AACTCTGTTT CCAGACTTCT TTCTGTTTGT CTTCAACTGC TTTCGCATGA	120
	AGRACCCCC AGGCTATTTT TCTTACCCGC CTGGTGTTTG TCTATATACC CGGTTGTATT	180
30	TITIGATAAAA AACTCAGCTC TITCCTCTACG GCAGAAATAT ATATCCAGTC CITAGCGCCA	240
	TGOCAAAATC TGOCTTTTTA COSCTGTTTC TOOCAGTCTT AGCACTGOCA GAAAAAAGAT	300
35	GTATOCOGTA TAGGCCCTGG CCCCGCGGAA AAAAAAAAAA AATAGAAAAA TAGAAAAATA	360
	AAAAGACTTG GGCCGCCCCG CGGGCAGACG AAGAAAAAAT AGGCGCCCAC CCCTCCAAGC	420
40	AGACCACAGG CGAGACATAA TAAAATCOCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC	480
	COGCCTCAT ACCCTGCCAT TCTGTTCCAT COGCCTTGCA AACCCAGTAG TGGCATGTCA	540
45	AASCATTOCT COGACGCTCC GCTGCCTTGC AGTCCACATC CTCTTCCTAA CCCCAGCCAG	600
	ACTICCCATA CITICCACIT CACATAGCAT ATCACITIC AGATCACIAC GIGACATICG	660
50	GTACKHATG GCACTCCAAT GCCGACAACC TCTTCCTACC CGTGACTTAC CCGATGTGCC	720
	AACTA	725
55	(2) INFORMATION FOR SEQ ID NO:1052:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LEWIH: 704 base pairs	
	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1641UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1052:	
20	GATCOBOTIAG TGAGOCCUT GGICAGACOC GOCAAGTGIG CUTGIGGICT GICCICOGCG	60
25	CCTTOCTCCT COOCACOCAC TOCTTOCOGIG CTCTGTCGTA CACCOCCTTG GTACACCATC	120
25	TCTGGTCGTC GCTTGCTACA ATTAACGATC AACTTAGAAC TGGTACGGAC AAGGGGAAITC	180
30	TGACTGTCTA ATTAAAACAT AGCATTGCGA TGGTCAGAAA GTGATGTTGA COCAATGTGA	240
	THTCTGCCCA GIGCTCTGAA TGTCAAAGTG AAGAAATTCA ACCAAGCGCG GGTAAACGGC	300
35	GOGAGTAACT ATGACTCTCT TAAGGTAGCC AAATGCCTCG TCATCTAATT AGTGACGCGC	360
	ATGAATGGAT TAACGAGATT COCACTGTOC CTATCTACTA TCTAGCGAAA CCACAGCCAA	420
40	GOGAACGOOC TIGOCACAAT CAGOOGOGAA AGAAGACOCT GITGAGCTTG ACTCTAGTTT	480
	GACATTOTICA AGAGACATAG AGGGTGTAGA ATRAGTGGGA GCTTGGGGGC CAGTGAAATA	540
45	CCACTACCIT TATAGITICI TIACITATIC AAITAAGOGG AGCIGGAATT CATTITICCAC	600
	CTTCTAACAT TTAAAGICCT ATACGGGCTG ATCCGGGTTG AAGACATTGT CAGGTGGGGA	660
50	GTTTGGCTGG GGCGGCACAT CTGTTAAACG ATAACGCACA TGTC	704
	(2) INFORMATION FOR SEQ ID NO:1053:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 678 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1642RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1053:	
	GATCOCCETT TOCCAACOCC TTOCTTCOCCA CAAAACACAG GGITCGAAGT TACATACTCT	60
20	TCAAGAAATT GACGAGGCCT TGAAAGCGCT GGAGCTIACGC GGGTCAGGGA MTGATGGTIAA	120
	TOCCTCATAT AAGTGCAACT GCCAGGCCAC TATGCATCCT CTTTTTGAGC TAGCCCCAAA	180
25	TIGOCIGAAC TGIGGCAAAA TTATATGITG COGAGAAGGI CITCATATGG ATTCCTGCAG	240
	TTATTGTGGG ACGCTGCTGA TACCGAAGCA GCAGCAGCGG GATATACAGA AGGTGTTGCA	300
30	GCCCCAACGC GAATTGGTAA AAGCCAAGAG ACAAGAGACC GGCTGGACTG GCAAGAACAA	360
<i>35</i>	GCAAAAGGIC TITAAGATTT GGAAGGCAAA GGGGAGAAAT ATGITCAGTG AGCAAGAGAG	420
33	GCTATTOGAC AAACTTGACA GGCAGCGGGA CGTGAAATGA AACGCAACCA GGTACTTGGG	480
40	GCAGAGGACT GTCTCAGGAG GAGGACTCGA TTCTGAAGGC TGAGGAAGTC GATCCGGAAC	540
70	TAACCCCCCC CACCCCCCCT TOGAGAATCT ATTCCACTITT CAAGACACTIA COGAACACAG	600
45	GACTAAAATA ATAGATACTG CCAGTGACTA CAGTATGTCA AACGACGCAG CAATTTGGGG	660
	GTCCCCATAT GAGAAGCC	678
50	(2) INFORMATION FOR SEQ ID NO:1054:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs	
55	(B) TYPE: nucleic acid	
-	(C) STRANDEINESS: single	

	(D) TOPOLOGY: linear	
5	(11) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1642UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1054:	
15	CATCTOSTAC COGSTACSST GCGGGAGCTT GCGGGGGGA GCCGGGGGCT GCGCTGCTTC	60
	TOUGCOGACA GOOGGCAAA TACOGUGTTO TACAAGCTGC ATGGATGGCT GOCACAGGCC	120
20	GTGCGTGTTG CGACGCTGCG GCACTTCTCC TCACACGCTG CGGCAACCGG GGGCAAGCAC	180
ne.	CTGGTCCTGT TTTGTACCGA CGTCGCCTCG CGTGGCTTGG ACCTGCCGGC TGTCAGCACT	240
2 5	GICATOGAÇA TOGACOCCCC CITOSOGGIC GAGGACCATO TOCATOGIAT COGGCGCACC	300
30	OCCUSIONIC STIGICANTICS CRASTICISTICS CTICTTONICS TOCCOGOGIA GCAACAGGC	360
	TACATOSAAC ACATCOSTOC CCACCACCUT CGTOSCTOGG ASCTOCTTOG CTACGATCGA	420
35	CACCTACTOS COCCOCCTT COCCCCCCT CTCCCCCCCT CCCACCCTCC CACCACCCA	480
	ACCIGACICOS COTOCIACAS CAACICOCACA ACTTOCICACO TICAACITOCA GOCCOSTIGIT	540
40	OCTOGAAGAC CCTCCOCGAA GGATCTTIOCC ATCAAGGGCT ACACCAGCCA TATCCOGCGCA	600
	TACGCAACCC ACATCTCTCA GCAAAAAGGG CTTCTTCAAC GTTGGCTGTC TGCATCTTGG	660
45	CCACCTIGGGG AAAGCCTTTIG GACTTIGGGGA GGGGGGCAAA GCA	70:
	(2) INFORMATION FOR SEQ ID NO:1055:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 616 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
cc	(D) TOPOLOGI. TITEME	

(ii) MOLECULE TYPE: DNA (genomic)

_	(vi) ORIGINAL SOURCE:	
5	(A) ORGANISM: PAG1643RP	
10	100 TO 10	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1055:	
	CATCOGAACA AGGAGCAGCA GTOCCATOCAG CTGTOGCAGC AGCAGCAGGG CACACTGCAG	60
15	GACAGGAAGC GGACATIACCA AGTCATGTCT CTCCAGAGGG ACAGGAGGGT GACCAAGTTC	120
	AAGCTICGACG ACTICCATICAG CAAGCGTTTC GAGTTCATGA ACAAGCCGAA GGCCAAGCCC	180
20		
	COCACOCCC CCCCCCACCACCACC ACCCCTCCAA TGCCCTCCGC CCCCCCAAC	240
	COCCOTOCIACA ACCOCAAGGT GCAGCAGGCC CGCCGCCGGG CCGGCCAGGC CGATTICGGCG	300
	COCCOCALA ACCCAMAGE GLACAGOC GEGORGO GGRANGE GALLOSSO	300
25	AAGCAGAGTA ATACGCCCAG GSGACTTCGG TGCGCTCGGA GAAGACCAAT CGCTGCAGGA	360
	ATTCCTGTOG CAGTCCGAGA TTAAGAGOGA TCTGTTOGAA CTGGAGGAGC AGAACGACGA	420
30		
	GAGOGCAAGO TOCAACAAGG AGAAOGTAOO COOGAGOTOO TOGTOGGTGT TOCAGOAGCA	480
		540
35	SCITCISCOC ACAGATATGG ACGACTITIT CAACCTCGAC CTCGACCATA TGAAGAACAC	540
	CGATGATGAG TOGTTOCAGG GOCTGTTOGG CACTCCTCGG GACGCGACCA CCTGCAACAC	600
	CATGCCCATC GAGGAC	616
40		
	(2) INFORMATION FOR SEQ ID NO:1056;	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 538 base pairs (B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50		
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1643UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1056:	
5	GATOGTIGCA AACAAGCIAT TACGGTGTCT ACACGTTOGA GAACAGCGCC CGATGCCATA	60
	TOCCACACOG COGOTGTCAA ACGOGTOTOT GGGCACGAGC GCTGACGGGG GGAGCGCCCC	120
10	AGGGCTGGCG CAGCAGGCGC CCGCAAAATC GTACTACCCG CTGGTGCCGG ACGGCCCACA	180
	GCTCACGCCG CCACTGCTGC CCGTGTCCAC GCCCGGCGAT GACGCCGGCC TCTACCGCTA	240
15	CCACAAGCAG ATCAGCAAGT CGTTCCAGGA CGACCTGATC TACTGCCCGC GCGCGCTGCT	300
	GAGCAAAGTC GAGCTGACGC AGTGCTACCA OCTGGACATG CTGCTGCTGA TGGAGCAGCA	360
20	GCAGCAGGCC CAGCCGAGTG TCAAGTTCAA CCCATATACG TCGCAGAGCT TCAACCCCGC	420
	GGGCCCCGCA TCGCCCGCCT CCTAGGGCCCG GCGGGCCCCCC CGGGACCATT TAGTTCCACN	480
25	GAATCNCTAT GICAAGACTG ACCCTTOCTC GCATCCCGCT TTATGTTTIA TTCCAGIT	538
	(2) INFORMATION FOR SEQ ID NO:1057:	
30	(5) COMMAND CARDACTED COMPAND	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 560 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(sell optomity overse)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1644RP	
	(A) CARCALLON, EMOLOGIC	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1057:	
50	GATCCTTTGC AAATTCGTCC ATAGGAATGT AAACGGACCT GCCCTCCCAC CTCTTGGTAT	60
	TOCARACAGE CATCUTGAGU TOGUTUGGOC AUTOCATCUT TADAUGCUGU TCUTCATCGC	120

	AMBICALATT TICGICTICT TCCGGCTTCT CAAAAACAAC CITATGCACT CTCTCAGTAA	180
5	TATACACAGE GTACOGOGTIC GCCGTCCCTG AACATTAGGA AGAACCAGCC AAATGGGCCT	240
	GTGCCTGGCG ACTGGCCGGA CTTCTGCACK AAATCCCCACC TCAAGTATAT GACCATCAAG	300
10	TOCCTGAACC GCGTGCTAAA CTGCTGGTAT GTTGTGTGCA TATCTAGCGG ACCGGCAGCT	360
	ASCERATIOGG TRICCOGCAC TICCARTAGG TRATCOCCCC CCGTTTGCAR CCCATGCTAT	420
15	ACCCTAGTAA CITTGCCTGC AAACTCAATA TGGGGCTTGG GCTTTTTCCA GTGGGCCTGG	480
	TTTGIAATTG GTATCAATGT CTGCCGAGAT GAGATGGAGC TGTCGCTCGA AGATATGTCC	540
20	TTTAGCAGGT TATOGTCTTC	560
	(2) INFORMATION FOR SEQ ID NO:1058:	
25		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 706 base pairs	
	(B) TYPE: mxcleic acid	
••	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(i) optomb	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1645RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1058:	
45	CATCTTOGAA GAGGAGGACT ATTCAAGTAA AATOGCACGG COCCAAGATA AGATGGAAGA	60
	GCAGTGGATA CGAAAGTACG AGCGTGAGAA GAAGAAGAGA AAGAGAGOCG CATAATCCCC	120
50	AGTGTAATAA ATCAATTCCG CCGGTTCGCT GCGCTGTAGC ATAATAATAT GTAGGATAGT	180
	GGTCAGATAA GGTATTICAA AAGTTAGGCA ACCCATGAAA CATCAAACTT TTCAATGCAA	240
55	TCATATGTAA GTTGCATATA TTACGAGCTG TCAAATAGAG AAACTCAAAT GAATACTTTT	300

	ALCALACCAT AACAAACOCA CAATGITACG ACAATGAAGA CCATAATGCA GCTTGAATAG	360
5	TOCCACCATG GOGCCATATG GTACCTACTG AACAGCAGAA GCAAGCTAAA OGAGCTCAGC	420
	ATGAGGGACA CCACTAGAGA TACCAGGATC AACGCTGTGA TATAATTACT ACCTTCAAAC	480
10	TCAGTCTGGT CATTTCCAAG AGGGCTGAAC AATGAAAAACA TGATTCCCAC AGTGGTACCT	540
	GTGGTTATGC AAGATACGAG CAGGGTGGTC AGGTAAAAACA ATGAGACCAC CTCATGGTGC	600
15	TIGIATCCAT ATAGGACATC AAGITCATCG TAACATACTA GCGCAGCCTC GTCATCCCAG	660
	THIGGAACIT GCAGITGGCT ACCACTCCCG GCAACGTGCT TIGCAC	706
20	(2) INFORMATION FOR SEQ ID NO:1059:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
	, -,	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1645UP	
35		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1059:	
	CATCAGCOGC GOCTGCGCGC GCTGTTGCCGC TAGCGCTGCA GCAAGCTGGC GCGGGCGCCCC	60
45	CONTINUES CONTROCATIC CONTROCACC CONTROCACT CONTROLITATE CONTROLINASC	120
	TOCASCOCCE TOCCETTOSC ACTICATOACE TEATOCACCE TECTECOCTIC COCCECCECC	180
50	CTGTCCGGCG CCGCCGGCGC CTCGCCGGCC GCGCCATCGC CGCGGTACAC ACGGCTCTTC	240
	GCATCGTACC CCGTCTCCTC GCCCCCCACG TCGTCGAGGT ACCGCCCCCG GTCATGCCGC	300
55	GEOCOGATOG CAGOOGCOCC CAGGOOGCOC GGOGGOCC GCGGGTGCAG TGCCAACTTG	360

	TACCETTOCA CTECTECCEC COCCTCCTCT CCCCCTCCCC GCCCCTCCCC CCCCCCCCC	420
5	GCCACTGCCG GCGCCACCGG CCCCTCGAAC CCGTACCATC GGTCCCGCTT GGCCTCAAAG	480
	CTCAGCCCAT TCTCCTCCCC GACCTGAAAC GCGCCCTCCC CACCATCCCC CCGCCCCTCT	540
10	THEOGREECC GCAGCAGOCA GICGOGCCCG TCATGATTIGG CGCCGCAGIT TOGIGCACCG	600
	COCCECTICOS CECCOCOCOCO COCCECCOCOCOCA AAAAACGETCA CITATTACOG	660
15	AACCTOCTGA GCCACOGAGA AGTCCTGAGC GCCCTCGCCG GGCTC	705
	(2) INFORMATION FOR SEQ ID NO:1060:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
25	(D) TOPOLOGY: linear	
	(_,	
	(ii) MOLECULE TYPE: DNA (genomic)	
<i>30</i>	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1646RP	
35		
55		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1060:	
	CATOGRADAC COCATOGRACO ACANGOOCAA COTOGRATO CTOGOGTOCO OCTOGOGTOC	60
40	GATCHANE COCATOLING MEMBECCAN COTOGOGNE CTOGOGNECO OCTOGOGNOC	00
	CATTICCTIC CICAACCACA TCGACCCCC GAAGIACAAC CICACCGIGG IGICCCCACG	120
45	GAACTACTTC CTGTTCACGC CGCTGCTGCC CTCGACGCC GTGGGCACGG TGGACGAGAA	180
	GTOCATCATO GAGOOGGTOG TGAACTTTOC GCTCAAGAAG AAGGGTAAGG TGTCTTACTA	240
50	CCACCOCAC COCACCTOCA TCAACCCOCA GOOCAACACG CTCACCATCA ACTOOCTICTO	300
	GACGETIAGCA CAGCTIGTICGC ACCCGGACAA CCACCTIGGGG CTGACGCAGC AGGACTICGGC	360
<i>55</i>	GENECIGNAG TACCACTACC TOGTGTCTGC GGTGGGCCGG GAGCCCAACA CGTTCGGCAT	420

	TOURRESTIG GARLARGARG GLAACITITT GAARGARATE CCALACITGT TOGAGATCAG	480
5	AAAGCGCTTC CTGTGGAAAGG TGGAGAAGGC GAAGCTGTTG CCCAAGGGGG ACCCGGAGAG	540
	AAAGCCTCTG CTGACCATCG TGGTCGTGGG GGGTGGTCCT ACCGGTGTGG ACACGCGGG	600
10	TGACTOCAGE ACTIACETOGA COAGGACOTE AAGAGATTCA TGCCCTCCAT COCTGAGGAG	660
	GTOCAGATICC ACCTRGTOGA GOCCTTGCCC AACGTGCTGA ACATGT	706
15	(2) INFORMATION FOR SEQ ID NO:1061:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 657 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDHINESS: single	
	(D) TOPCLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1646UP	
30		
35	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:1061:	
	GATCAAATOG GITIAGCCCGT CTCCAACCAG CCCTGCAACA TAGTGCCAGT AGCGGTCGTA	60
40	GEOCEOGRAFIC GEOCECARACE COCECARACET ARACTECTOG TOCKGRAFIGE AGECTIGOCRE	120
	SCCSTTSCCC ATCTTGTGTG TGATGTCTGC AATCACCTGC TGGTACTCGG GCTTCAGCTT	180
45	GIGGAACTOG GOTAGAATOG TOCTGAACTO CACCAGCACG TOACGGTOCT TOTCOGTOTT	240
	COCCUTOCCE TOGARACTOC ACCUATOCAG CUTCAGUITC TOGICGAACT COCCCAGUAG	300
50	CONCACCITT ACCITONGAC TGATOGICAT ATCGTCTTCA ACAGTATCCA GONCACOCAG	360
	AATCAGGTAG AACAGCATCA CCGCGTTGGG CAGCTGGGGA TGTAGCTGCA TTATCACGGC	420
55	OCCARANCAC TOGRAGICOG CIGIAGORGO TOGIAGORGO GOTTGAGOCIO TOCACAGOCOC	480

	TOCGTOTOGT CCCCAGGATA AAGCCGTTCC CTCAGAAATT TGAGCTTCAG AGCTGCCTTC	540
5	AGCTCCAGTG GGTGTGTGAA TAATTGAACA ACCTTCCCCA TGGTCAGGAT TGGATTAAGT	600
	AATTGCCAAT TATGTCAAGC GCCTGTCAGT TGGTGATGTC GCGCTTGCTT GTACAGG	657
10	(2) INFORMATION FOR SEQ ID NO:1062:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 727 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1647RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1062:	
	CATCCASCIA CATACCGIGO CAATIOCIGA TAAATCCTGO CAGAATGCCA TAACCCCTCT	60
35	CLEAVACECE CYACGOCLICE GEAGGECCYC CYCLLELLOC CYCYLLOCCYC GCCLLCLECYC	120
	TOGATOCACA ACTAATATTG AATTCAGTAT CCCGCAGTAG GOGGGTACAT AACTGCTTAC	180
40	GIACTOCCAC TACGACACTG CGCCCCCCAC GCTGCACGTG CGATGCGGCT TACAAAGACC	240
	AAGICCTTGG CAACACCIGG ATATGGTATC CATOGGGGTC TCTGAGGACG GCGAGATTCT	300
45	TGATAGACCC CTTGTTGTAG COCAACTCCC ACTOCAGGTC COGGTACGTC TCCTGGATGT	360
	CAGCICAAAG AGGCGCAGGG TCACTGAGGG ACACACCCAT GTGGCTGTAC CCCGTGGGCT	420
50	CTGCGTTCCC GTTGTGATAC GAGAAGTCGG CGTCATCCTC GGTCCCCCAA TTGTGCGTCA	480
	CCTCCAGAAT CCTCTCCCCC TTCAACCCCT CCTCCCCTCC	540
5 <i>5</i>	COGTGAATIT COCATTIOCG TOCTOOCTICA CCTCCAGTAG CGACATACCT ASCACATTCT	600

	GOTAGARICE CARCACTIC GUIGCUICCU TCACACGUAG CATOGUGUGG TUAAACTUGG	660
5	GOCCCAGGIC CACTOGCTCC GOGTCOGACA AGTTGTACTG TATCAACTCA ATCCAGTATC	720
	CGTCGGG	727
10	(2) INFORMATION FOR SEQ ID NO:1063:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 615 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1647UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1063:	
30	GATOCCAGCA CGGTGCGGGT GCAACAGAGG AAATATATGG CACTACAGAC AGTGCACAGA	60
35	TECAGGACT COUCOCCTG COCCOCCAC COTATOTICA COCCOCGA ACCGAAAACC	120
	TAGACTOGGC AATACGGGAC CTTGCATTGT TAGAAGAAGA OGTAAAGAAG TACGGATGGG	180
40	ACAACCTGAC GCAACGGGAG CGAAGAGAGA TTGGGACCAA GCGGCAGCTC GTGCAAATTG	240
	TGCCCCCCC CCATGCCCCC GCCCCCCCCC CCCACCCC ATTCCCATATC CCCCCCCCC	300
45	CCGTTGTCGA GCCTACTGCG CCCCACGAGA ACACCTGGGA GCAGCACCAG GTGCAAAAAG	360
	COGTIOCOCCC CGAGGGGGCC TCOGACATAA TTGAGGTGGA CCCCTCTGAA CAGTAGGAGT	420
50	TIGITCTOCA CTCCCCGTCC GITGTCCCCT TTACAGAGGA AGAGACCCTG CCTCCCCCCC	480
	AGCGTGTCCA GAAGCAGCTC GAACAGAAGC TCGAGAAGGA AATTAAGCGC GTGGCGTCGA	540
55	TICANGNANC TANGAGGCAG CITCCIGIGI ATGCGIACCG CGACGAGCII CIGAAGGCGG	600

	TGCGCGACCA CCAGT	615
5	(2) INFORMATION FOR SEQ ID NO:1064:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 648 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1648RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1064:	
	GATCCACCTC ATGCAGIGCG CGATTOCÁGC CCIGCCIGIC GITTAAAGIC TIGAAGIAGI	60
30	TOGTOCTICAA ATOCTTIGTICA AATTTIGTIACA GGTATOGTTT CGAAGATTTIC GAGAATAGTC	120
	CTTCCACCAC TTTCAATGGG TTCTCCTCGA ACTTGTCGAG GAATGAATTC TCCAGCTTGG	180
35	AGAATGCATG CTGTGAAGAG TATATACGAG ACCCAGCTTT CGCCACGAAT TTGATGAGCT	240
	CATTGAAGTC GITTOCOCATG TOOCTCTOOG GTATGAATOG TOOCACAGTC AGCGTCAAAG	300
40	CTCCCTCCCT CATACGACCG TATCCTCCCCC GTCCCTACTC GTCCACATCC AAGTTATCAA	360
	GCAGATAGAA ATCCTTGATT TIGCCCTTGT CTGCGAGAGA CCGCAGGTIAC GCCAGGAAAA	420
45	GETGETACAS COCCETTCCC COSTTACCET AGAICTTGTT CAGAATAAST TOSTOGTOST	480
	TOCCTICATE GITGGCATCE TIGTACTETT CTACCGCCTT GCAAGAGGGG AAACACACCT	540
50	GOCCCGCGGT GAATATTAAG TOCATCTGCG TCGTCTTCTC CACCAACAGG TCCGTACGCC	600
	CAACGATCGT CACCAGGATT TOCAGAAAAG CGTAAGTCGT GCACATGT	648
55	(2) INFORMATION FOR SEQ ID NO:1065:	

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 715 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) CRGANISM: PAG1648UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1065:	
ro To	GATCTAGCAG GTGTTGAACA GATAATGGAA TGGCTCTCCT ATATTCCAGC TAAACGTAAT	60
05	ATGCCCGTIAC CTATACTGCA GTCAGAGGAC AACTGGGATA GGGATGTTGA ATACACACCA	120
25	ACACTICACA GOCTTATGAT GIACOCTOGA TGATTGAAGG COGCCAAGGA COTGATGGAT	180
30	TIGARTATOG TOTGITTGAC AAGOGITCCT TOCAGGAAAC ATTATCAGOC TOGOGGAGAG	240
••	GOGTOGITGT AGGCAGAGCT COCATGGGTG GIATCOCCCT CGGTGTTATT GCCGTTCACA	300
<i>35</i>	CTOTIACAAT TGAAACTGTG ATOCCTOCCG ATOCCGCCAAA COCTGCATCC ACAGAAACTT	360
	TGATTCAGGA GOCAGOCITTA GITTGGTTATC CTAACTCAGC ATTTAAAACT GOGCAGOCCA	420
40	TAGCTGATTT CAACCACGGA GAACAACTTC CACTCATGAT ATTAGCAAAC TGGAGAGGGT	480
	TTICTOGTOG TCAAAGAGAT ATGITCAATG AGGTCITGAA ATATOGCTCC TTCATTGITG	540
45	ATOCICIAGI OCATTATAAA CAOCCIGIAT TOGIATACAT ACCIOCAACA OGIGAGITGA	600
	CARCITOCITIC CIRCUTTICITO GIRCATCCITA CAATITAACTO TICACCAGAIG GACATGITATG	660
50	CICATICOGA CICOCOCCA OGIGIOCIAG AACCIOCIGG TATOGITOGI ATAAA	715
	(2) INFORMATION FOR SEQ ID NO:1066:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGIH: 714 base pairs(B) TYPE: nucleic acid

5	(C) STRANDEDNESS: single	
J	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1649RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1066:	
20	GATCAAAOGC AAAACTGTGA COCAGAAAAA AGTTTCGCTG ACAGACGACA TGCTCGCAGG	60
	OCACCAGOGG GTGGGCAACG GAGGGGTTGGC GTTTCCAGGG ATGGACCTGG GGGGGACCAC	120
25	GAATCITTIG CIAAACAACA CIATCAACAA GACCAAGITE AGICACCIAA AAAAACGCGT	180
	AGATAGTATO GAACTOCATA ACCAGCAGOT GOGOGOAGAG AACAATAGTT TGAAAATOGA	240
30	ATTOCAAAAG ATGAGTTOCA GATATAACTO CATGGTGGAG AACCTGGTGT CTCTTAAAAA	300
	CTACAATAAT TCCCTCGTTG AGAACTTCAA TCTGCTGGTTA TCCACGCTGG CGCAACAGGG	360
35	CCTGAAGGIT CCCCATCCAT TAAACCTOGG CAACTATGCA TCTTCACAGG TTGCCAAAAA	420
	TICATCIGCT TOOGACGITC AACOSCATGT ATOSCOGITG GGTACTGTAG CACCTAGGAA	480
40	CATACCCTTG GCGCAGGCTA CCCCGTCGAA AGAAGAGGCC AATCCTCCTA CAAGCCTGCG	540
	CCCAGCTTC CATGTTCTGC TOGTAGAAGA ATGATTCGGT TTGTATCCAA CTATGTTGCA	600
45	AATTOTTGAG AAAATATOGO TGTTCGGTGG AAGTOGTAAC GGACGGCCTA TCTGCTAITIG	660
	AAACAGTAGA GAAATTOCAG TACGACCTOG TICTGATOGA TATOGTGATG COCA	714
50	(2) INFORMATION FOR SEQ ID NO:1067:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 663 base pairs	
	(B) TYPE: mucleic acid	

(C) STRANDEDNESS: single(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) Original Source: (A) Organism: Pag1649UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1067:	
	GATOGOTIGGO GOGGICAGOO ACATIGOGGOG GOATITICADO TITOTADOSACA TIGOAATOTIAT	60
20	GBCGGCTGTG CCCCGCTTGC GCCCGCAGGG GAAGTACGGG CTGCCCCAGC CCCCAGCCCA	120
	GOCACCACOG COOOCGITOC COGACGIGGA TGIGGIGGIG ATGCCCOGGIC TAGGGITCIG	180
25	COCCEATACE GOCOCOCCE TOCCACCOCG GOCAGOTIAC TACCACAACT ATGTAAGOOG	240
	TACGCAGCAG CTGCACGGCA GGAGACGGCT GCTGGTTGGG CTGGGGCTCA GCCAGCAGCT	300
30	CATGITICCAC GICCOCCIAG ACCCCCACGA CCAGIGCTIG GACCCCGGC CCTGCCCCCA	360
	COGACAGTIG AGGIGGGGGC ANCOCCCCC COGGGAGATA GTIGATATAT AAGTGTATCT	420
35	ASSOCIATIAGE GAAGCTCCCE TECOCACOCA CENATGECCG COEGCOOCTC TOGETECATCA	480
	TOTOGROCTIC CACACOGACG TIGHTOCCGT OGTOCTOGAC GOGGGTGGTG COCACCACAA	540
40	CGAACTGGTT COCCAGGGTC GOGAAACAAT ACAAGATCTT GATGTGCTCG GTTACCTCCT	600
	AATCOSTOCC GSTCACGAAT GTGACTGCCT CCCGCATCAG GTGGCTCAGC ACCGTGGCCA	660
45	GGA	663
	(2) INFORMATION FOR SEQ ID NO:1068:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1650RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1068:	
15	GATCOCTCTG CCCCCACTCG ATTITTGTCC ACCCCCCACC CAACAAGGAC CTTCCGTCCA	60
	TCATGUAÇÃO CITOGOGOTOG ACAGGUGAÇO CGAAGGGUGT GUCGUTGAÇO CACGGUAAÇÃ	120
20	TOGTGGCGGG CATTGGCGGT GTTTCCGTTG TCATCAACCG CGCCATTGTG AAGCCTGACG	180
	ATCGIGICAT COCGITCITG COGCTTGOGC ATATTTTTIGA GCTTGIGITIC GAGITIGACCT	240
25	GICTOTACTO GOOGOCTTA ATTOCCTACO GCTCCGTCAA GACGITGAGC GAGOCITCGG	300
	TCCGCAACTG TAACCCCCAC ATGAAGGAGT TCCGGCCGTC CGTCATGGTC GGTGTCGCAG	360
30	CTETCTEGGA GOSTETCAGE AAGOCTATTE TTGCGCAGGT CACTAAGTTE CCTCCGTTCA	420
	AGCAAAAGAT ATTCTGGGGG GCCTACCACA CCAAGCTAGG CATGAAGAAG TGCCACATTC	480
35	CAGGCGGGGA TCTAATAGGA AGCATGATCT TTAAGAAGGT GCGTGAGACC ACTGGTGGCA	540
	ACCITOGCTA CATCTIGAAT GGIGGCICIC CATTGIGGGG GCATACGCAA GTITITATIT	600
40	CCAACTICAT TICCCCCCIC TICATICCIT ACCCCTIAAC CCACACTGIG CCCAATCCCT	660
	GTATAGTGCC TCCACACCAC TTCAAGTACG GGGTTGTGGG AGACAT	706
45	(2) INFORMATION FOR SEQ ID NO:1069:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 674 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (Genemic)	

(vi) ORIGINAL SOURCE:

	(A) ORGANISM: PAG1650UP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1069:	
10	CATOCATTIC TCATGCACAT TAACGCTATA TGCGAGGAAA GCAATAACAA GAAGCAAGCC	60
	AAGAAGICIG TTAACTICIC TATGCTAGGG TTGACTGATT TTACCAAACT CAAAAAAGCC	120
15	GATACTACAG ATGTCTGGAG AGGGTTTAGG ATGTACGAGG AAGTACAAAT GAAAAAGAGA	180
	TTTAGTTATA AATGGGATTA TGATAAAGIG TOCAGGGAAT TGGATGAAGA GACATGGAAT	240
20	AAGATTATTA ATAGGGAAAC TITIGAATI'IA TITIGCATI'AG TIGGAAAGATA TAGGGTAAAG	300
0E	ATTGAAAACG ATGCCAATAT AACCTATTGG AGITCTGTCG TTATGCGCAA CTCCTGTCGC	360
25	AAGCATGAGG CTACAGGAGT GAGGCAATTGT GCCAACTTCT TCTGTGGTAA ATGGGAAGAC	42 0
30	CACCCGAAGC AGTITICCCAA GTGCCGCCGT TGCAAGCGCA CAAAATATTIG CAGTTGTCAG	480
	TGICAACTAC AATCTTGGGC ATATCATCGG TACTGGTGGC ATGATGTTGG CTCTGTCTTC	540
35	ACCIOCACCT CUTUAACCICO AAACACCACT COCCACATA COCCAAATOC TUTUCGTCAG	600
	TOGOCTOGAA COACGACCAC TACTACCACG GOGGCTACGG AGGTAGATCA ATOCATTITG	660
40	ATGACAGCAA GOOG	674
	(2) INFORMATION FOR SEQ ID NO:1070:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 622 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1651RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1070:	
10	GATGGCGACG TITIACCGAAG AGCAAAAAGA AAAGTACGCG ATGGCGTTGA AGCACAAGGG	60
	GAACGAGIGC TITIAACGACC AGCGGIFACGA GGAGGCGATC AAGTTCTIACG ACTGCGCGTT	120
15	GAACCIAAAA GAACACCCCG TEFTICTVACTC GAATCCCGTCC GCGTCCTACG TCCCCTTCAA	180
	CAAGCTIGGAG AAGGTTIGTIGG AGGACACCAC TIGCTIGCACTA AAGCTIGAAAC COGACTATTIC	240
20	TAAGIGITIG CITOGIOGIG CAACAGCTAA TGAATOGITG GGIAATTATG CTGATGCTAT	300
	GITOGATTIA TOTOCCGIAT CICTATACGG CGGGIACAGC TOGCAGACAA TIGAGCCCGT	360
25	SCTOGASCOG AATATGAACA ASCAGSCTAT SCAAGTATTG AAACAGAAAC TCTCTGGTGG	420
	AGAGAAACAC GAACTIOCIT CCAATACTIC CTTAGOGICT TICTICOGCA TCTTOCCTIC	480
30	GEAGACATOS TIGGAGAACT AGGATGAAAC TIGGGAAGCA GACOGCATTC TICTCAAGGG	540
	ATTOTOCOCC CTACACOCCC GCCAGGCAGG CTCCTATGAA ATTOCTGATG AAGCCTTTAC	600
35	CGATCCTCTA CAAAACTTCA CC	622
	(2) INFORMATION FOR SEQ ID NO:1071:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 679 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1651UP

55

	(XI) SEQUENCE DESCRIPTION: SEQ III NO:10/1:	
5	GATCGTGATT TTCGCGGGCT GCATCCTGCA GGCTCCACAT CATGCCGTGC GCCAGGCTAT	60
	OCTGAACATC CCCAGCGGGG TCTACTGCAC GTTCCGTGGG CAGTCATCGC CTGCGATCCA	120
10	GTACGGTATC TOGICTACAA ACTICATCAC ACACGTGAAT GAGATOGAAA OOOCAGACCT	180
	GGACCOCTIT CTCGAGGTGG TACGCACGAT ACCAGACAAC ACCTACTGTA AAATCCGTCT	240
15	TOTGACCTTC GACAACGTGC CTTTTGCTAT CTCCCTGAAG ACAAACTACC ACTACTTCCC	300
	CACCASCEAG CTCTCCCCCA ACTCCCGACAC CGGCCGGCTGG ATTGAGCACC TCTGCAACGC	360
20	TACCCCCCCT AAAAACTAGC AATAGACTGA TATCTCTTAT AGAACGTATA AACTATTCAC	420
	ATGTAACCCG ATCACGTGAC GAGCOCTOCA COCAGCTCGT GCAGCATCCT CAGTGGTATG	480
25	GCAGTAGGCG CCGCAGACGC TTCAGATGGG CACTCGCCGC CATGGTCCGC CCAGAGAGCT	540
	SCTTCASCOC GCGCTGTCCC ASCCTGTGTT ACCGTGGCTG CGGCCASCCT TCGAACGCTT	600
30	GIACCICCIG CAGICIICOG CCAICICITA GCIGOGCCIT IGIGOGICIT CATTAGIGIC	660
	COCACCATGA TCAGCGACG	679
35	(2) INFORMATION FOR SEQ ID NO:1072:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 692 base pairs	
÷∂	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1652RP	
50		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1072:

	GATCTICGIT CGIGAAAACC TIGCACGICT TCATCACCIC AAGAAITIGCC TCTGCATCTA	60
5	TICTOTOCOG TIOCATICIG CCITCCITAT TGICCICAAT CATGCGCGCA AAAGCGCGCG	120
	GCGTCCAGTC ATGACGGGAT CGGCCCTTAT AGGACTTCCC TGCAAGCCGC ATGAGGCTCC	180
10	GCCAGCCATT TICTICAATA ATATIGACAA GTCCTICGIT TTCCAACACG ACCTIGITCG	240
	CGAGACIGIG GAACGIGTIC ACGICTATCT GCTCAAGTAT TICTACCCTT TCCTCAGCAG	300
15	ACCATCOCAA GITOCAATCT GOCTCTTOGA ATGTCTCCAT AAGCTTTTCA TIGATGTTAT	360
	CCACTOCTTT ATTIGTCAAG GAGAGCATTA GTATTTCATT AGGAGCTACA ATCCCTTCGT	420
20	AAACCAGGIT GIAGACITTA TGCAGTAGIG TCACGGICTT GCCAGACCCA GGTCCCGCTA	480
	CCACATTGAC AGTIGTACAA GECTCATATG GATGTGTTAC TACTOGTGAT TGGGACGTGG	540
25	TCAGIGCTTT CATTCATGIA TGATACATGC TCGAGCGTCG GCCAACGAAA TAAATTCGTG	600
	AATTTOOGTT TTAACATACT CAAAAGAAAT GAGATAACOG CCCCCAAGGG COGAGTAGAA	660
30	TTACAGCAGC TATTGAATAT ATTTAGITTA TT	6 9 2
	(2) INFORMATION FOR SEQ ID NO:1073:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 697 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1652UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1073:	
55	GATCICCCCA CCATICICCI CCAGCGCCIT CIGINAGCGI TCCCGGCGIT GCICICICCC	60

	THE PROPERTY OF THE PROPERTY O	120
5	CTTCTTCCAC TGTTTCTTCC ATTGCGACTT CGACATGCCT TCGGGAACGG GCGGCAAGGC	180
	ASCCCGTGGT TTTGGCCGAC TCAATGTTTC ATCATTATTA GTTTCAGGAG TCATTGCCCA	240
10	GITTICAGGAC TCTTAGCOCA AGGICTIGIC ACTGAAGTAC AGTAAAATGG ATGCCCTTTC	300
	SCOGTIGATICA COCAATICACC TGGTIGAAATT TYTICGCCCAT GGTICAGOCTG TATTAGTICGTC	360
15	ACGIGACAAC AGIITCAGCCC ATATAIGGAG CCCCTAGGIC ATATAAAGGG TCAGGAGCCC	420
	GCEAAAGICT TIGIATICIG ACCIPITATI GCGGAGCTIT AGGGCGIGIG TCTCTATCCA	480
20	GAGCCETCTC CTCAAAACCC TCTCACCTCA CCCCGTTCTA CTACACTCAG ATTTAAAAAC	540
	CAACAGOGAA GCAGCAGAGT ATGAGGTCCT TAGCAACTAA ACTGGAACTT CCATGGGTTG	600
25	AGAAGIACCG CCCGAAGCIG CIGAAAGAIG TGIGGGAAAC GAWGAAACGG TGCAGCGCCT	660
	GCAACAGATC CCAGGGATGG AAATATOCCA CACTTGA	697
30	(2) INFORMATION FOR SEQ ID NO:1074:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 707 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1653RP	
5 <i>0</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1074:	
	GATCTTTCAT CCTATTTCGT ACCTTAAGGG CTGTTCCGTG CTGGAGATGA TCTCCGGCTA	60
55	TATAGGGGAG ACCGICTICC TGAAGGGTGT TGCCTTATAT ATAAAGCGGA ATAAGTTTGG	120

180

CAATOCTACC ATGGAGGACC TGTTTGGGGC CATTAGTGAG GTAGCAGGCC TTGATCTCAT

5	GOCGAAGOCA AAAGATTOGA TICTAAAGAT COOGTACCOG GITICTOGACA TCACTGTTGT	240
	TGATGGGAAG ATTTCACTIGT CACAGAGAGG GTACCTTTCG AGCGGACAAG CTGACGCCAA	300
10	TGACGACCTA ACCACCTGGT GGATTCCCCT GGAACTGACA CAGGACTCAA CTTGCACTAC	360
	AACAGAAATG GTTTCTAAAT COCAAGAAAC AGAGATCTCA GCTACGGATT TTGTGTTCTT	420
15	TAACAACGAT GOCCACGGCT TCTTCCGGGT GCATTATGAG GATGAGACTA TTCTGGCTAA	480
	CATCHOCAAG AACATAGOOC ACCHGICCTC ACGCAGIAAA ATTGCGTTAA TTTCGGATGT	540
20	TOATGCCACT GGTACCTTCA COCAACTCAT GGCTGTTCTG TCTGCATTCT CTGCAACGCA	600
	THOSCAACAC TACTATOTTA TOCAACTOTG CATTOTOCAT THTOCACTOG GOOTOCTCAA	660
25	TCATATATOS CSATGOGIOS CAGAGATOOS CAAGAAGOTT GOGGOST	707
	(2) INFORMATION FOR SEQ ID NO:1075:	
30		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 689 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1653UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1075:	
50	GATCTANTAC TOSCIACCCAC TOSCICTITET GOCOGTISTCT ATCTIGTATOC GAACCAGCGA	60
	GECTETEATE CAGACANATT STACTACEAT GETTECCOCC TCATTECTET GAACESCOCA	120
55	GPTGTGGCCC AAGGCTCGCA GITTTCGCTG AGGGATGTCG AAGTGGTTAC TGCAACTGTA	180

	ATTACON PROBLEM TO STAND TO STAND THE CONTROL OF TH	240
5	TOGANTANOG TOACITIOGA ACGINITICAN GINCOIGING ANCTOGCOCC GATOCANGAT	300
	AGGITICAATIC CTACGATTAA CCTGACGAAG GCGAAAGCCC CATACTATICA CAGCCCAGAG	360
10	GAAGAGATTG COCTOCCCCC ACCTTGTTCG TTATCCCACT ACCTACGTCG TTCCACACCA	420
	ACAGGCTAIT TTCTTCCACT ATCTGGGGGC ATTGACTCAT GTGCCACTGC TGTAATTGTG	480
15	CACTUTATOT GICOGATOGT TGICAACGAA ACATUTGAGG GIAATUTGCA AGIAATTGCA	540
	CATOCCACAA CATTOCCTOC TOCTACCCAT CACTOCATTC CAACCCATOC ACCTCAATTT	600
20	GCAAATATGA TATTICACAC TIGITTIATG GGAACAGCAA ACTOCACAAA TGAGACTOGC	660
	AGTCGGGCAA AGAAACTTGC GGAACACCT	689
25	(2) INFORMATION FOR SEQ ID NO:1076:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 598 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(D) TOPOLOGI: III BAI	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1654RP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1076;	
	GATCPTATTA ATTITICATICS TOCTATATTC TAAATTCAAG TAATCATAGC GOGTGATGCG	60
50	GTACGTACCT ATACATATAA COCACAGTTC TCCATCGTCT ATGCGTGTAT GAAAATCACT	120
	CCAGCCGIGC GACACGCCAC GIGIAATCIA GIGAGTTICA AGITCITCCI CCICATCGGC	180
55	AGAAAGITOG COODCOOCG TGAGGITCTT GAGCCGCTCC TTGAGCTGCG QGATAAGGCT	240

	ATTOTOGET TOAGCATGCA TOCOGATACO CTOTAGAGAC ATATGAGOGG AATOTGCACO	300
5	ATCTAAACCA TGTTCGCTGT TGCTGCCAGT GGCAGCTGCC AGTTTGGGAC TGGACAGACC	360
	TGTCTGTCCA TCTTTGTAAG AATCCTCGGT CGTTGCCCAG TTGGAATTCA TGGTTCCCAT	420
10	AGIGIGCAAG ATTITICTCCT CTTCTGTTAG TTCCAGATGG GTACCTGTCA GATTGATCAA	480
	GCACCTICCCG CTITTIACCCC CCCACACCTT CCCCACAACA CAGTICCCCCC CTTCCCCTCC	540
15	CITICACCAAG GITTIGTAATIG GAGGIGTGAG ATCTCGGAGT CCTTGGTAGT CTCAGACA	598
	(2) INFORMATION FOR SEQ ID NO:1077:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 571 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
25		
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1654UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1077:	
40	GATCOSSSCC GOGTCOSCSG CAACCAACGA TGTCACGTGT GCATACCAGC GACCTGGTAG	60
	GCGTTACGGT GGCAGCAGCA GCGGTTGCCC GAAAACCGGC AGCAGAGCAA GTACTGCCTG	120
45	AAGTGGGGGC CGTATCTGTC GGAGCGGAGC TGGGGCACGG TGCGGCAGGA CTACTCGTTT	180
	CACCERCIACE CETICOCCECA CITICOCCETTO CASCACROCCA ATGCCCCCCET CITICOCCETCE	240
50	GOCCAGGACG GCATCTICGG CGTCAGCCAC AACCGGCAGC TGGTGTGCCT GAACGTGGGG	300
	ATGTGCAACG GOCGTGACGA GCTGCTCAAG GAAGCGCATG TTCGGGCTGA CCCGGCCCCA	360
55	GGGCAACCAC GGGGAGGACT GCAAGGAGCT GTACTACTAC CTGGACAACC TTCCGGAGCCA	420

	TECGLACATE AAGGCCCTGT AYAAGTACCC GNICAAGCGG GCGTTCCCGT ACCAGGAGCT	480
5	TATTGCCCCC AACGACCCCC CCCCCTACCC CGACCCCCAC CTCCACCTGT ACGAACTTGA	540
	CGGGCTGTAC CGCGAGGCGG GGACGGGGGGA C	571
10	(2) INFORMATION FOR SEQ ID NO:1078:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 694 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1655RP	
25	(A) CATALLEY. PARTOSAF	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1078:	
30	The suggestion and the state of the state of	
	GATOCACTIT CCACTCIGAC ATOGGTCAAT CAACGCTGGG CACTCAGGIT CAGTTCIGAA	60
35	OCANTIOCAG TOCCOGCAGI TACCOTTONT TINITIAGAG ACTIAGIGGI GITATAAGIC	120
	AGTOCTATOG AACAGOTOTO GACAGTOATO GGAAACGAGA AGITACOOGO COTTGAGACA	180
40	CAATCTGTTA CCCCACTTTG ATTTACATGC GTTACCCGCT CTGGGTCACG TGCCGGCAAG	240
,-	CACATGACAA AGGCOGAGAG CTAGTTACGT GAGGCTCATT GGGGTATGCC GGAAACTCTA	300
45	ATGACTAGAT CATCOGAGAA GCACCOGTAT ATAAGACGCA TCACGGTGGT GCTGGAGAGA	360
	GIGIGIAAAA TOOCAATTOC TI'AGCCACTG ATGCCAAATA CACTGGATAA GAGITACGTA	420
50	CAAAACGOCC CTTGGAGGGA CGGGGTGTTC CAAGGGAAAG TGGTCTTCGT CACTGGCGGG	480
	GCCGGCACCA TCTGCAGOGT GCAGOCGGG GCAATGGTGC TACTTGGTGC CAAGGCTGCG	540
55	ATCATTOSSC SCAATGISSA GAAGACTAAG AAGSCGCAG CGGAGATCCC SGAGTTGGGC	600

	GACTOSSCIG ACTOCGIGCT COGNATIONS BACGIGGACT TCCGGCAGGT CCCGAACATG	660
5	AAAGGGCGCC GTGCAACACA CCCTTGCCGC GTTT	694
	(2) INFORMATION FOR SEQ ID NO: 1079:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 675 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1655UP	
25		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:1079:	
30	GATCTCTCTG ACCOCCCCA AACGCTGCTC CGCGCACATT GACACTGGTG TTACCACCCA	60
	TTATGICGGC GGCCGITTCA TCCCAGATGC CCIGGCCCGT CGTCATGGTT TIGATCCGTT	120
<i>35</i>	CCCGUACTOT GOCACCGATO AAATACTGOG TATTTGAGTG CATATTGCTT TATTCTATAG	180
	TCTGCGTACA TAAGCCCGGG TTTCAGAGGG CGGGTAACGA TGACGCGTAA CGTTTCTTTT	240
40	TOGREATATE TAAAAAGAAA TETECAAACA TTTTTCATGA CATGAACGIT ATACTGGCTT	300
	GTTTCTCTCT TGAAGTCAGC AATCTCTAAC CTTTGAAGGT GATTAATAGG CTGTTGCGTC	360
45	GIGITGEAAC ATTGACOGAG CITTCCTTGT TGTAAGCGAT TAATCIGTGT TGCCAGTTTC	420
	ACTITICIOGA ACTOGIAGCA GGICTGACOG GICTGOCAAG GGOGIOGGAG ACTIGCAAAT	480
50	ATAGOCCCAA GACAACCTOC GAGATACAGG GCAGCTOCTG CAGCCAACAG GTGGAGTGCA	540
	COCCGATCIT GAGGACTAGC TOCTICTOGGA CCAGATGOCG AAGGAAAGCC TOCGGATAGG	600
55	CGTAGCAAGC ACGGAGCCCA ACGGGFIGAA GGTGFTCATC CTGGAAGACA GCCAGTGCAG	660

	AGACACTORG ACTOR	675
5	(2) INFORMATION FOR SEQ ID NO:1080:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORCANISM: PAGL656RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1080:	
	GATCTAGGGA TCAATGGCAG CTAACAGATG CTCTGACATT ATGCATGAGC GCAATCATGA	60
30	TOGACACATC GAAGCTCAAG CATAAAGIAG AGGACTOGGA CATGCAAGOG TACGCCATCT	120
	GCAAAAAGOGT GITGACCAAT ATGAACGAGG ATGOGTACTA CAAGOGCATG AAGGCAGCAA	180
35	AGAATGACCT AGATGCCTTC TCACTCGATG AGATTCTTCG TAAGGACTAT AAAGAGTTCG	240
	TGITCCCCAG CCCCAGTGCA GATCTACGTG TTGGCGTACC TACTGTCGTG CCCTCTTTCG	300
40	AATOGATGOG OGAGAAGTTC GOOGACAATG GGACTAOGAA GCTCTGGCAC AGTTTCCTTC	360
	TOGACCATAA GITAGATTIC CTCGTGGTGC TCACAATTAA GAAGGCCAAC GAGGGTTTGA	420
45	AACCEGGAGTT GECTATCATG GCCAACTCCT GCGACCGTGC GCACCAGGTC GAGTTCTTGA	480
	TOCANAGOUT CACCOCAGAG TIGCAGTIGA GCAAGACCIC IGICTICICC COOSSCICAC	540
50	TOGICATIGA GACGIÇOGAC CAGAGAATIGO TATOTIQUOAG TOGICAAGOAA ATAGTACOTO	600
	TOCTCAAGAG AACOGTOGOC GAGTIATIAGC ATGCTTATGT AACTAACGIT CCAGTTACCA	660
55	TCTTCCCACA TCTCAGCGGC AATGTCGCGT TTGTGGTCTC CAACC	705

	(2) INFORMATION FOR SEQ ID NO:1081:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 670 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1656UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1081:	
25	GATCTCTTCC TACCCTGTAT TTCTACTTAG CAGGAACCTA AATATGTCGA AATCATCGCT	60
	AGTAGGATGT TTTTTCTACA ACACAGACAT TTACGCCAAC CAGAACGCTA ACGCATGCAG	120
30	TATCTCCCCCC ACHATCTCCC TACCATCCCC GTAATCCTAA TACTCCTTCC CCCACACCCCT	180
	COTCACOTTO AACTOCCAAA ATTOCCTOCC CATACOTTCA CTGTCACAGT AAATOCACCG	240
35	COCCACGIGA TOCAATTOOC CIGICACGIT CATOCOCTAG COCCGCCCC TATTAGACAC	300
	TCCCAAGGIG CATTIGAGGI CCGGCTGAAG GCGGTGAATG GGACTGAGGG CCGGGGCCG	360
40	CACTICACTA TOCTOCCIOC AGAGGACGOG TGGGGGCCGAA AAGACCTGGC GCGTGCTGAA	420
	CTGCCCTGCC CGCCGTGCCA CCGCCTGCTG GTTACGGCCC AACATGCAGG CCCGTGAGCG	480
45	OGATIGOCCTIC OGAGTITITIGG ACGGAGCTIGA TIGGACTIACTIG GCACTIGOCAC AAGOCTIGOGG	540
	ACCACTOTOC GGCCCACAG CAGTACCTGA CGAAATATAA CGCCCTGCTG CCTGCCGCACG	600
50	GOGRACOTOCT GETGGGGGAC ACATTOCTCA COCTOGGGGA GGGTCTGCTG TCAGAGAAGC	660
	TOOCGATGAG	670

(2) INFORMATION FOR SEQ ID NO:1082:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 620 base pairs	
	(B) TYPE: nucleic acid	
5	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1657RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1082:	
20	GATOGATITA GATITOACCT TOAGGCACAC TAAGAGATGG ACTOCTTACA CTAAGGGTGG	60
	OCTOLOGOCO COOCTIGARO GIGITITICOT CORCOCROR ACTIGICATICIT TRACCOCTICA	120
25	CCTAGTACCA TCTCCAGCTC TAGGTGAGGC CGTTGTACCT ACTTCAAACA ATTACACTTC	180
	CACTCCTCTA TIGAACOCOG ACCCATIGCA CACCTITGIT CCACCTICTA GCTCOCGTAA	240
<i>30</i>	GAAGCGGITC TCCTTCTCCC GCGAGCGGGG AAACTCGTTT GCTTCAGCTG GTGACCACCA	300
nc.	GGAAGCIGIT ATCCACCAAC COCTOGAACA AAGGITGATG TCTTCAAGOC CACCAAAGGA	360
35	CONTINUOCO CONNENTOCO TONGAGAGOOT AGIOCGIGOG CACANTOCAT TONGAGAAAG	420
40	GAATATCITA TOTGITAACO AATTCAAACG TTOGGACTTC CACGOCTTGT TOGCTGTGC	480
	CCAAGAGCTG CGTGCCGCTG TCGAGAGAGA GGGCGTTCTC GAATTGATGA AGGGCCCCCT	540
45	CTTGACGACC ATATTCTATG AGCCATCAAC GCGCACATCC TCCTCTTTTA TCGCGGCAAT	600
	GGAGCGCCTC GGTGGTAGAA	620
50	(2) INFORMATION FOR SEQ ID NO:1083:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 578 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1657UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1083:	
15	GATICAAGTOC TITOCAGOOGA GOCCAGTICTOG CACOGCATTAC CAGAAATIGCA TITOGCISCACC	60
	TACCOCCATA TICTOCCCC TGTACTCCGT CCACGAAAAG GCCCAGCGGT GTGCCCAACGC	120
20	AAAGGCTACC ATCTCCAAAC AGAGGCCCAC ATTGTGGTAC ACGTAGCCCA TGTTGGTGCC	180
25	CSCGCAGTCC TGAATCACGT TCAGGTAGTG GAGAAGCGTG ATRACCATAC CCTGCCAGTA	240
23	GGATGCAAAA ATGATCAACT TAACACATAA GAATTTAGGC CATGGGTTGT ACTTGCGCAA	300
30	CTOGFTGTAC AAGCACTTCC AGAACACCCC CAAGTTATAG AGCGACCATG ACCCCCTCCC	360
	GITGTATACA AGOGTCAACC ACTUACATOC CAGATOOCAC TOCAACACOT GGAACGCAGA	420
35	CATCCCCAAG CAGTACACCG GCTTGAACCA CACGTACTGT AGAATGCCCC GCTTCACAGC	480
	CAATAACGCC TIGGGGICCG CCATAITOGAC CATGGGCAAC ACCCAACGIC CCACAACGGG	540
40	AATCOGGTOC TOGATCCTTT TCTGCTCCGG CGCAAGGT	578
	(2) INFORMATION FOR SEQ ID NO: 1084:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGIH: 693 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
55	(A) ORCANISM: PAG1659RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1084:	
5	GATCAAAACT TCATTAAACT AATAAAACAA TTATTTTATG TATATTCATT GTATAGTCAT	60
	TTTCAGACAA AAATOGIOGA AATTTTAGOG GOCAAACATA AAAGTCAGAC ATTAGAAACT	120
10	GACAGATACT TEATTEACTG CATAATTACA CTAAAAAACAA CTGTTCTCAA AAACTACOGA	180
	THATTGACCG CCCCCTCACT AATAATGTAC TCCTTCTATC GGTTTCTTGC GGGTAGAAGC	240
15	ACCIAAACAG ATCAGTTICA CITTOCAATT TOOGCACTTT TACCITTOCA CTTAACCATC	300
	ATTCTAGTGT ATTTTATGAC CAGGAAAGAA AAGGAGCCTA AAAACCTGAA GOCAGCCAGA	360
20	CCAGCGACIG ATCCCAAGAC AAAAACCAAA TATTIGITAT TAGAGGITTC TICAGGIGAG	420
	TATATTTGGG TTATCATCAT GATCAAAATC AAATTGGAAA GCATCCATAA CATGACAATT	480
25	CTAGICCOCA CATCACOGTA GIGATCIOCT TGCTTTTOGA TAGGATCAAC TTTTATTTCT	540
	ACCACITICAT COCATITIAG ACCACCITICA TITICCIOGIA TITIATTATOG ATGIOCTIGIG	600
30	SCCATTCAGT ACCCTCAACT ATTIGTTIGC CACGGGGGCCC TGGGTAACCA TAGCTTCAGA	660
	CITIGGCTIC CACCOCIGOS AACCOCCTTT TCT	693
35	(2) INFORMATION FOR SEQ ID NO:1085:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGIH: 726 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) CRGANISM: PAG1659UP	

(ix)	SEQUENCE	DESCRIPTION:	SEQ	\mathbf{m}	NO:1085:
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;	GATOGAGIOG TOCACCAGGI	AGICCTGGCC	CGGCTTCACG	TTCCCCCCCCC	TOGAGAAGIA	60
	GACCCCGGTAC TGCTTGCACG	CCTTCTTCAC	CTCCTCGTAG	CTGCCCGTCA	GCCCCACCAT	120
0	GICCOCCTOG AACTOCCCA	GGTACTCCTT	CAGCACCCC	GGGGGGTTCCC	GCGCAGGGTC	180
	GCACGTCACG AAGATICGGCT	GCACGTCGAT	coccognici	TTCAGTCCCC	GTAGCCACGC	240
5	CCCCASCITIC TCCACCICCC	CAGGGCAGAT	GTCCGGGCAG	TGCGTGAAAC	CGAAGTIACAC	300
	CAGCGAGAAC CGCCCGAGAA	GETTETTETE	CCTCAACTCG	TIGCCGITGA	AGTOCACCAG	360
o	CTGCAACCCC CCGCCCACCC	000000000000000000000000000000000000000	GIACOCCOGG	TTCGCCTCCG	CCTCCCCCTC	420
	CACCTOCAGE OGEOGETTET	CCCCCCCAAAA	CACGUAGAAC	AGCCCGCCGC	CCP/GCP/CAGC	480
5	AGCACCGCCC CCGCCTTCCA	CCTCCTCAAC	TOGATODOCC	OCCOCTOGAC	COCTGOCAGT	540
	CONTINUENTS COCCCCACC	GGGATCCGGC	TCAACGGCCG	CCCCTTCCCC	66050GIGIG	600
o	eccaecase: ecclociete	TOSCOAGCCG	TGTTCGCCAG	AACTCCCCCA	CCCCGCCAAA	660
	OGCIGOTOTO TOCCITOCAA	TTCCCCCAGC	TTGCCTGCAA	ACACCGAGTC	CTACTGATCA	720
5	TCTCTG					726

(2) INFORMATION FOR SEQ ID NO:1086:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 720 base pairs

(B) TYPE: nucleic acid

(C) SIRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1660RP

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(xi)	SEQUENCE	DESCRIPTION:	SEQ	\mathbf{m}	NO:1086:
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5	CATCAATICG	ATGCCAACCA	AGATGAAGAC	CATCTOOGTG	AGITAGCAGT	OCACTOTOOG	60
	CATACATOGT	CIGAGACGGA	TAGGAATCIA	ATTTTCAAAT	TATTOGGCAA	GITCAAGAAT	120
10	ATCAAAOCTA	TTTACAAATC	CCAACATGTC	COCCAAAGGT	TGATGGAATT	ATTOGGTAGT	180
	CGAACCCTCG	AAGTGCAGAA	ACTOGCCCTA	CATCCCTTCT	TAGCATACAA	GGATCCAGTA	240
15	OCTGTGAAAT	ATAGOGACAA	TCTGAAGAAC	TTATTAGATG	ACACGITATT	CAACGACGAA	300
	GTAACAAAGT	TATTTOCTCA	GAATGAGTCA	AGGITATIG	TCAACACTGA	TCAAAGATTA	360
20	TTAATGCCCT	TCATTTTGCG	TETETTEAT	GGCCGTGTTC	AGACACCTAA	TACCAGTGGG	420
	ATCAAAAAGA	CAAGAAAAAC	TOCOGICATA	ACTGTOCTGC	CAAATTTAGG	TGAGAAGAAT	480
25	ATTACTGACT	TCTTGGCTCT	GGGTAGTAAT	GGTATCAACT	ACCAGTACTT	CITTIGAAGAG	540
	AATOCGGITA	TTCCTGACAG	TGAGCITACA	GCCATAAATT	TTAGGAGAAT	GCTTGGCTTC	600
30	ATAAATGTCC	TAAGIGCCIC	GITGAAIGIT	TTAGGITCCA	ATTTCCCGGA	GGCGGTCAAG	660
	ACAACTATTA	AACCTCTCGT	TTACCCAATT	CACATGICAG	GICGIACIGG	ACAGAATAAA	720

(2) INFORMATION FOR SEQ ID NO:1087:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
- 50 (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: PAG1660UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1087:

5	GATCTTATAG ATTITICATOC CCAAGCITAC AAAGAGAACG TTATCCACCT GITTTAGCCA	60
	GOCTIOCATG TATTITICAA TOGIACCCAT GITCTCCTGG CCCAAGITCT TGAACAAGIT	120
10	AGITAGIACO AGACIAGOCA TOTICCIGCA TITIAGGAGAG TOGICATITA CIGATACGIT	180
	TECTAGGAAC ACGAAGAATG ACGATGAAAG TITICATTAGT AAAGCGGCCC CAGATTTIGTT	240
15	CATCAGAAGG TTAAGCAATT CCATAACAGA TTGAGCACCT TCTTGAGATG GATACTGCAA	300
	ATIGITGACT AAAAATTICA ATIGITTITIC CAGCCIGOOT TIACITIGAT CATATICCAT	360
20	GAACAACTOG TAATAGACAC TOCTOGCAAC ATCCCTGATT TOCTTAGCAT GATTOGTGAC	420
	CATGACTTCT GCAACGITAT CAATAATATC GTACAGCTTC GGAAGAACAA TATGTTTGGA	480
25	AACCAAGGAT TICAAAAATC CAAAAGCCAG ACCITGCITA TIGGGCTOCA TCAAATCIGG	540
	TTCAATCCGA CCCAAAACAT ATTCGAGCGC AGAATCCTTT AATTCAATGT CTTTATAGCG	600
30	GATTAAGCOCA GATTAAAAACT TCAGACOGAC TTGACAAAGT TCACCAGAAG T	651
	(2) INFORMATION FOR SEQ ID NO:1088:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 96 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1663RP	
ю		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1088:	
5	CATCGCCCTT TCATCTCCCC ATACTTCATC ACCGATGCGA AGGCCAACAA GGTGCAATTC	60

	GAGAAGCCAC TGTTGCTTTT GTCCGAGAAG AAGATC	96
5	(2) INFORMATION FOR SEQ ID NO:1089:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 583 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1664RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1089:	
23	GATOCTIAGGG TOGTTCATOG CACTGAGCOG GACGTGTTCT TOGACCOGGTC GAACCGCAGC	60
30	AAGAGTOTGA AGTOOTTGAA COOGTOTOTG GAGCOOCTGA AGCOCAATOG GCAGGOOGG	120
	TOGRITITICO CAGAGOSCAC GOSGITOGIAC ACAACGCAGA TOCAGCIGOT GOCATICAAG	180
35	AAGGGGGCGT TCCACCIGGC GCAACAGGCG CAGATTCCGG TGATTCCGGT TGTGATGTGC	240
	AACACGAGCA COGTIGTICAA CCCGGGGCTG GGCATCTITTA ACCGCGGCAC GATCACGGGG	300
40	AAAGTOCTOG AGCCGATCGA CACGGCTAAC ATGACCAAGG ATGACGTGGA CAAGCTTGTG	360
	ACCIGACITICO ACCICAAAAT CICATICOCICAG TITOGAGGOOD TITOGOTIACISC CICTICOCATIC	420
45	GTOGACACCA GOCTACCOCA ACAGOGGTG COSCOSCAGT TTGTGGACTG CAAGGAAGAC	480
	ATCACOGAGG TAACOCOCCT CTCGAAGTAA CCTTGGTTGG TATCATATAA ACGTTGCGAC	540
50	GASTIATOTA CATATAGCOC TOCTAAGTAG GCATTCAGTC CCC	583
	(2) INFORMATION FOR SEQ ID NO:1090:	
	(i) SEQUENCE CHARACTERISTICS:	
5 5	(A) LENGIH: 598 base pairs	

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1664UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1090:	
2 0	GATCCCACTG ACCGTGAATA GCCCACCGTA GCATGCCCCC CTCAGCCCCC TGCCCAACCA	60
	TAGCAGOGT CCTTCCGAGG CTCTGGTGGC CAAGACAAGG ATCCACTGGC CCACCACGCC	120
25	CAGUAGGAGG ACTIGOCCACT GGACTIGACAT OGTOGACACA COGTUGUIGA TIGCAGAGGTIC	180
	AATTATCAAG CCCGACAGGA AGCGCGAGCA CGTCGAGGCA ATCGCAAAIT CTGGCAGCAC	240
30	CCACCCTICG CCCAACAGC TOCACACCCA GCCCATGTTG GTGAGGAACA TCTCCATCCG	300
	OCCCAGOGAC AATIAGCAACA CAAGGGCCCAT GAAGTACGCC GCTGGGTCGT GGAAGAAGTT	360
3 5	COCCACOGG COCCGCATGT CCTGCCCCAG CACCGCCTCG GTGGGGCTCT CCATGCCCCC	420
	GAAGGICAGI GITGOGGCCT TGACCTTGAG CATAGTGACG ATGCTGGTGG CAAACCACAT	480
40	CCACAAGCTG ATCAGCGTAT ATCCGACAGC TAGAGTCCTG AATACACGAG AAAGGTCAAG	540
	GTACGGCAGG CCATTTOCAA AACCATGGTA TCTTCAGCAG CTGCGACCTA GCACAGAC	598
45	(2) INFORMATION FOR SEQ ID NO:1091:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 713 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1666RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1091:	
10	CATCUTUCG TACTAACACT TAGACTITAA TTAATAATAT TATTTGTAGA AGATAGAAAC	60
15	CATACTCACT CACGROGRAT TRACCCATC TCACGRAACC TITRAATTGA CGAACAGICA	120
	AACCCIACTT AGCTGTTACA ACCAAGAGGA TAGGITGAGT CGACATOGAG GTOGCAAACA	180
20	TAACTTACAA TAGCTACTCT ATOGTTATAT TACCCTGTTC AATTTTGTTA TCATAATAAC	240
	APPRACTAT TATTICAATA ATTOTCAPTA TIGITCAGAC TATTICATTA TGTATIATTT	300
25	ATTAATTAAT ACATATTOGG CITTOGIGGA TATAATTATT GITAATCCIA CICATATATC	360
	TAGTOGUEA ACCUTETAT AACTUTATAA AAACEATUGT TATAACCUUC GCUCAGATU	420
30	GICCTITATI ATIATAAAAT AATATTAGCA GITCTITGCA ATTAACCCAA TITACTCAAT	480
	ATATTAAAT ATTGATAATT AAATTTCACA ATTTAATGGG ACTATTAATT AATCCCTAGC	540
35	GIAACTITIA TIOGITAICA AATAOCATTA CAATATGIAT ATTITIGITO ATTATOOCAA	600
	ACTIACGITA TIGITCIACT TGIACGIATT ACAATTATAG CACAGITATA CCATTATATT	660
40	TATTTAATAT ATTATOOCTA TATTATGITT TATTAACATA TAAAACIGTA CAT	713
	(2) INFORMATION FOR SEQ ID NO:1092:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) IENGTH: 677 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1666UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1092:	
5	GATCCTTATA AAATOOOCAA TAGACGTGTT ATAATATAAT ATACAAAATT ATAAATAAAT	60
	TIATITAA AAATAAATTA AAATAATAA GIATTATAA AAATAATAA ATTATITAA	120
10	AATAAGIATG GATTTITAAC TGAAATTTGI TAAAATGAAA TAAGAATTGC TAGTAATCTA	180
	TIAATAAGAA AGTAATGGTG AATACTCIAA CTGTTTUGCA CHAATCACTC ATCACGGTT	240
15	GAAACATATA ATTAAATAAA GAATATTAAT TAATTTAATA ATTATTAATT ATTATTAATA	300
	TTATTTAATA AATAAATAA ATATTTTAAT TTAAATTATG AATTAATGOG AAGTGAAAT	360
20	ACAGITACIG TAGGGGAACC TGCAGIGGGC TTATAAATAT CITTAATATT CCATTITITAT	420
	AATTAAAAT TOTTTTAA TATTTTTAA TATTTTTAA TATTTTAATAA TATTTTAAAAAT TOTTTTAAAAAT TATTTTTAAAAA TATTTTTAA TATTTTAAAAA TATTTTTAA TATTTTAAAAA TATTTTTAA TATTTTAAAAA TATTTTTAA TATTTTAAAAA TATTTTTAA TATTTTAAAAAA	480
25	ATTATAATTT AATAATTTAA TAACTTATTA ATTAGAGAGT TAGGGTACAT CCCCCCTAAT	540
	GCTATGCATT ATGGTTGGTA CCACTCTAAT TAATAAACTA TAATAAATAA ATACTAATAT	600
30	TITATATAA TIAATTATA ATTATTITT ATTAATATTI TAATATTATT TAATGAAATA	660
	TATAAATAAA GIATTAT	677
35	(2) INFORMATION FOR SEQ ID NO:1093:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGIH: 707 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1667RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1093:	
5	CATCCATCGT GGTGTCGTTC ATTACCTGTA ATTCCATTCA TATCCTGGCT ATGCAGTGCT	60
	GGAAACGCTC CTCCAGCGCC TCTATTTTGT TATTCAGCTC CAAGTACTCC GCCAGCTTAA	120
10	AGGICAACGA GAGOGACCCI GCATTGCACC TGACGGCGAT CTCAAGGACC TTCTCGTGCT	180
	CONTENDED CACAAACANG COGNACTIGN ACCATANCIC COOCCAAAG CACANGICCT	240
15	GCACAGOCTG GCGGTGCACG TATTICCACGC GCTGGCGCAG CACGACTTGG GGCAGGTGGA	300
	CONTRINGIC CASCIDOCAC TOGATOCACT TOGICCAGAT CTOCAGCIDG TACTCATOGT	360
20	ACTGACCOGG CGCAGGCAGG TICTGCTGTG TCGCCTGGTT TAGCTTCGTG GGCAGCGAGC	420
	GCCGCAGGCC CTTCGTCAGG TTCGACCACT CCTCGTACAG CGAGCGCCCA TTCATGTAGC	480
25	TOUCOGAGAG CTCTCCCCATG AACTTCCCCC CCGTCAACTG GITGACCTCC TECTCCCCACT	540
	COCTICIATIT CTCCCAGTAC COCTCCAGGG ACTCCACTGG CAGGCACAGC AAGGCGCTTG	600
30	TACASCITICE GEAGAATETE GACCESCETE TOCTOCTOCE ACTIOCTICAE CESCITICEAE	660
	TOCTOCAGAA ACTOCAGGTA GTOCTOCCAG AACTOCATOG ACCOCGG	707
35	(2) INFORMATION FOR SEQ ID NO:1094:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 723 base pairs	
40	(B) TYPE: nucleic acid (C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	

(A) ORGANISM: PAG1667UP

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1094:

(ii) MOLECULE TYPE: DNA (genomic)

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	CATCTAAGGE ATGGGTGACT GCTGCCGGTG CTCACAGCAG TGGCACGTAG CTAGTAATGG	60
5	TOCGARATCG ATCARAGAGG GTGCGTCTGG CGGTACAGGC AGARAGCACG CCCGCCGATA	120
	CANGUICCAG TICTACAAGC ACCIGCAGII CCAGGGIACG AGGIACCAGG TGGIGACTIC	180
10	COCCOCCETAT CICATACACC COTACCCCCA COCCAACCCC COCCACCATCA COTCOTTTGT	240
	CANCTICCATIC CATICOGAAAA TCAACGACGA TGTGACACGG ATCAGCGACG ACCOGGTGAC	300
15	OCACODOGIO TOGAAGTOGGA AGAAGTOGAA GCTGTTCCTG CTGCTGGTGA CGCTGTCGCA	360
	COCCECCO COCCACTACT COCTOCACAA CACCAACCCC TCCCACACCC CCCCCCCCCC	420
20	AGACGOCCC COCAAGAGC ACCAGGIGGA GCAGGCCCC ACCCGCCCCC	480
	CGICIGCACA CIGGIGGAGC AGATCATOCG CGAGAACATC ACCAGGACT ACCACGAGAG	540
25	CGIGCACCAC GAGAACTACG TGTTCTCGTC GATATGGGGG AACTTCATGG AGGGGTTGAT	600
	ANACCACTAC CTAGAGAAGG TCATCATACC CAAGTCCGAG CTGAAGGTGT GCCAGCAGCT	660
30	GTACCAAGCC GATGATGAAG ATCATCTCAC TCTATAACGA ATACAACGAG CTCATGGACA	720
	AGA	723
35	(2) INFORMATION FOR SEQ ID NO:1095:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1669RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1095:

	GATCAACAGC ACCTOCACCT GOGACAGGTC GAACTCATCG TAAAAAAGGCA GOGACGCGAT	60
5	ACCCTOGTICS GCCCCATICA CACCOCCATIC CACCATICACC GTCTTGCCCT TATACTGCAA	120
	TATATOSCAT GAGOGICCAA CCICATIGCT GCCCCCAAGC CCGAAGAATC GGAACGAATT	18 0
10	OGTATOTAAC TTCTCCTCOG TCATCCGCAA TTTGTTTATG TCTGCCTGCT GOGAGGTGCT	240
	GIOCTOTOTA COCAATOCOT GOGACACTOG CTACTGAGAC AATTCCACGT AGCTGCTGCT	300
15	SCAACTITIT TOCASCIATE GAAATACCSI GSITCGGIAG ATTIGATICI GIOGAGAIGA	360
	ACCATCAAAC GOGAACACTG GTTATCOGTG ATGOGTGTTG TTAGTACCCA ATCACCCCCA	420
20	GAGACAAGTG CCACTATTAA TIGTAGTACT TACAGGAACA COGATOGCAA GAACTCTTAA	480
	COOCTCCCTT TACCAACGAT CAACACTITT CTCCTCGAAC GITATCCTGT CCCCCCGGIGG	540
25	CGATTGCGAA TGATTGTTGA ATTGAACCAG AGAGCGGAAA ATTTTCGTTC TCACGTGACC	600
	GEATCHTACA TAAGCTACTG AACIATATGA AATACCGACG TTGCTCGAGG ACCGCTAGCG	660
30	CAGTIGUCICA AGCAGTIGATO ATGAGATTICA GITGITICTIGA TGTGT/ACATT CAGAGT/ACTIG	720
	œ	722
35	(2) INFORMATION FOR SEQ ID NO:1096:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGIH: 675 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) CRGANISM: PAG1669UP	

(xi) SEQUENCE DESCRIPTION; SEQ ID NO:1096:

	GATCAACAAG TOCAACAGCA AGGTOCAGIT OCOCCATGIG CCCTOGGGGA TOGTGATTGA	60
5	GTGCCAGGCA ACCCGCAGCC GCGAACAGAA CCGCAAGCTG GCCCGGGAGA ACCTAGCCGC	120
	COCCUTORICE CAGCOCCCCC CTIAGCOCCAG CCAACCCCAG CTIGGCCTTTCC OCACCTIGGCC	180
10	GCGGCAGGGT AAGCACGGCC AGGCGGCCAA GAGCCGCCGAG AAACACGAGC GCGCCCGCGC	240
	CCAACGOCAG GAGCTOGCGC GCGCCCCGA CGCGCAACTTC TGCGTCAGCT	300
15	CONCERNAGO CONCERNACIO DE CONCERNACIO ACCESCADO ACCESCAD	360
	GICTTITIOG GCAAITICCAA ATAGACACCC TAGTCOCCTC TGCTGCCCGC GAGCGCAGAG	420
20	CASSCASCIA GCACACCACC GTOCACSOSC ASCSCTTTIG CIGGOGAGIC GTOCCSCAGI	480
	COOCTGOCTC TOGTGTOCAC ATGCCGCTCC GGCGTGGCAC CGCAGTGCAG AGCTACCTAC	540
25	GTAGGITTGC AGGCTICGCA GTAGGCCTGA TACTGGCTCT GGTGAAACTT CCCGACAAGA	600
	GIAAAATCIC ACCAAAGAAC AAAAAGATAT GITAGIGAGG ATATCICACA TICTGITACT	660
30	GGAAGTACAC AAAGT	675
	(2) INFORMATION FOR SEQ ID NO:1097:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 697 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1670RP	
50		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:1097:	
5 <i>5</i>	GATCCOGCAA GATCGTCGTT CAGTTCACCG GCAGATTGAA CAAGTGCOGT GTCATCTCTC	60

	CHARACTCAN COTCANENTC MACGACOTCO NOMBIOGAL TOCCANECTA TICCONSCUA	120
5	GACAGTTOGG CTACGTCATC TIGACCACCT COGCOGGCAT TATGGACCAC GAGGAGGCCC	180
	ACAGAAAGCA CGITGCTGGT AAGATTTTGG GTTTTGTCTA CTAAGCCGCT GCTATATAGC	240
10	GIATUTACCT CTAATGIACG ATACTCAGTG TCTATTACGA CCCCCCCACCCCCC	300
	CACATACGAG GOCAGOOGGC GACGGCAAGC GGGAATTCAG ATGCGTTAAT TAGCAGTAGA	360
15	TUAGUAGUAT ATATGUACAA ACAGCATACA CATGAACGGC GICGCCGATC ATAATCUTCT	420
	ACCICITCTA CCACCCITCT TICIOGIAGA GIOCGATIGG ATAGGAGIGA OGIOCICGAT	480
20	ACGCCCCATT CTCAAGCCCC ATCTGGCCCAA AGCTCTCAAA GCAGCCTGAC CACCTGGACC	540
	TOCOCTICTE GICTTOCTAC CACOGGIAGC TOTCATOTIC ACGIGCACAG CACTGATGCC	600
25	GACCTCCTTA CACTTOOCAG CGACGTCCTG AGCAGCCAAC ATGGCAGCGT ATGGAGAGGA	660
	CTCGTCTCIG TCGGCCTTCA ACTTCATACC ACCGGTA	6 97
30	(2) INFORMATION FOR SEQ ID NO:1098:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1670UP	
45		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1098:	
	GATCTATTTG TOCCGTCCCC CATTAACCAA GCCCCCAACCA TCCATCCAAA TCATCACACT	60
55	ACCCTOSSCC THTCACTITIC CAAGCCTITIA TCAACAAATC TGGTACACCA TACATCCATC	120

	OCGACAGCAC ATATACCAGA ACGGGAAAGC CGACAAGATG GCACTAGACT CTGGTAGGTA	180
5	ATCIGAGITC GACCATATOC ACTICGITAA TOGTGATAGI TGATAAAAAG AAACGATACT	240
	GAAAATTITA ATGGITACCA ATCICATCTC ATCGCCATAC TGAAAGAATA TIGIAGGICT	30 0
10	COCACTOGAA CAAGGATCAA GOOCAGGCTA AGACAATAAT GGTTGCAGGG GAGGCAGTAC	360
	AGGAACTAGC CCCAGATGAA GAAGAACTGG CCTTGGCTAA GCTAGTGTTT GGCGACACAG	420
15	CAGACTITOCA TGAAGOOCTG OGAAATOCAG ACCTTAATTA TGITTICTICA GATGAAGACG	480
	TATATOCCCA GCAGTCGTOC AGTCATCACG AAGAAGGGAC TGAAATTOGT CACCTGAATG	540
20	ATGACCAATT GITTTITGIG GACGAAGGIG CAGATACCGA GGCAAGAGCA GATGGAGAAC	60 0
	COCAGGCCAT GEAGGTGGAC CAGGTTAGCG ACCAAAGCGA CTCCGGAGAG GAAAGCGGTA	660
25	GCAGCGCTGC ATGGTCACAT TCGGATGACG AACACTTAAA CGTTACAATA GGG	713
	(2) INFORMATION FOR SEQ ID NO:1099:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 743 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1671RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1099:	
50	GATCCCTTTC AAACCATCCT GTAACTACCC TGAACCACAC TTTACAAGAC AACCCCATAT	60
	CGACAATCAC AAGACTTOCT OGAGACATOC COGOCAOCAA TCTTCATOGT GTACTGACGG	120
55	ACTATAATCC AAGTOGCCAT TIGAATTOGC AGCATGATGC CACGCTTTCC AACCTGAGCT	180

	CGAAAACIGG AGAIGIACAI (CGCCTICCA ATTICCTCTIC CAGITITIAAI GGAGCACAAA	240
5	AAAGGCTAG CATCCCAAAT ATCTTAGGCT CTCCTCCACT TAGTAATCAA TCAAGAACTC	300
	CAGACAACOG TITTAACACAT OGTACATOGA TOCATGAGAA COCOCOGITTA GAATTAAACOG	360
10	GTGATCAGTC TITTACTCTTT GGCGGTAATA CAGGGCAGGC ATCGGGTAAC TTGGCGGGTG	420
	TTTCACCOOC CGAAAACTCC CGAAGGAGCA ATTCGCATGA TCAGAGCCAA TATAGATTAC	480
15	ATTCCAACGC TITCCATTCG ACTGCCCCTC CAAACGAACC TTCTAAGAAC ACTAGTCCAG	540
	GTACAACTGT TOCACCTOOG AGOGTTGTTG GTACAAACAC AAGGAACACA CAACGTGGAC	600
20	CCACGGGACA TGTCTCCCAA GAATCAGTCG AACAGCCGCA ATCAGCTTCG CGCCCATCCG	660
	ATCAATCTAG COCAACAATT ATCTCCCCTA CTCATCATAC CCACCCACTA CTCTCTTTT	720
25	CGACAATCIC TICTAACACA CGC	743
	(2) INFORMATION FOR SEQ ID NO: 1100:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 661 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1671UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1100:	
50	CATCAGOCAT GCGCAGCACA TTCCGGCGACG TTATCGGCGA GCACGACCTA CGCGTCTGCA	60
	ACTATGICAA GI'ACGCCAAG AAAGCTATTA AGGCCTTCGG CTTCTCGCCA GACGCATATA	120
55	TICAACAGAT CATCCAGCTA GCCATCTACA AGTATGTGGG CAGACAATTG CCAACCTACG	180

	ASSCIOSSIC ONCEASHAND TICTICANDS GLASSACCON ASCOSSOCIAC OSCISTICIC	240
5	COSCUTICOSC CAAGITTIGIG AAGACTTOSC AGTOSCOGGA AGCATOTOCA AGTGAGAAGA	300
	TIGCTOCTOT ACGIGAGICT OCTAAGAACC ATTOGTOGCT OCTAAAGATG GOOGGGACG	360
10	GCCAGGGIGT TGACCGCCAC TYCTTCGGTA TGAAGAACAT GTTGCGTGAT GGCGAGGAGC	420
	ATCCTCCACT CTTCCCCCCAC CCCCTGTTCC ACCACTCCTG CACGTGGTAT GTGTCTACCA	480
15	GICAGCIATO TICOGAGIAC TICOAGOGAT ACOSCIGGIO GCAGGIGAAC GAAAAIGGOT	540
	TIGGICTOCC GTACATGATC AACAATGACT GGTTACACAT CAACATTGTT ACMAAGCCTA	600
20	AGAAGTOGGG CTATAGTGTG CACGAGCTTT CACTACTACT TGACCGAAGC AGCAAACGAG	660
	A	661
25	(2) INFORMATION FOR SEQ ID NO:1101:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 623 base pairs	
30	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1672RP	
40	(A) Charlest. Institute	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1101:	
	CATCCTGTAT TIGTCAGGCC CATCCAAGCC CTCCCCCCCA CCCAAACCCCA CTATCATGGG	60
50	CAAGAAGTIGC TOCAAGGTIGG GATIGGGCAGC CTGCAACAGT TCTGGTGCCT CGGGGCTGGA	120
	CAACACACCA ACTACTCTOC CCAATTTACA GOCGTTGCGC GOCGTGCTTA CCACGACGTT	180
55	GGACAGTOCC CAGTGAAAGG CAGATGAGCG CGAGTGGCTT TTTGCGATGG CAGATCCGCA	240

	GAAGAGATOT CICAGGITGT GCACAGCCAT GCCAGACGIT ATTATCAACC CGCCGACGTC	300
5	GCGGTACCTG GACAGGAGGC GCCCGAGGCC ATACTGGTCC CGCAGGTCGT TTCCCGGCGGC	360
	CAGTGATATT TGGACCAGCG GTACCGGGAC ATCCCAATCG TCATCCACGC ACTICGAAGC	420
10	GCAGAACOCA ACTITIAGOS GGACCCAAAC GCCATOGICT ATGCCGCGIT CIGIGAGCAC	480
	AGOGCATAGO GGGCTGCGTA TGTGGTTGAT GGTGTCCGCG ATGTCGGTAA CTAAAGCCAT	540
15	GCTTGATTTG CTATGGAACT CCTCCTGGTA CATCCGGGTC GAGAACCCAT AAAAATCGTA	600
	TATCAATTCG TTCTCCAACG GGT	623
20		
	(2) INFORMATION FOR SEQ ID NO:1102:	
~ -	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 694 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1672UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1102:	
	GATCCCAGAT TAGATATTAC TTAAACGTTC CACAGCTTTT TGATGGCCTA GTTCTGCTGC	60
45	ACGICTATAA TOGTCCATCG CCCTGTGCAT GTCCGGGATGA CAGCCGACCG CGTGCTCCGT	120
	ATAGAAGCCC AAGOCATACT CCGCTTTCGG TAGCCGGCCT TCGGAAGCAA TGGATGCTTT	180
50	ATACOCCCAT TIGIAAGAIT CIGAAGCGIT GOGITCCAGC ACCCCCTIGA CACCAGITAG	240
	GTACCAACCA CTCAAAGCGA GCATAGCCAT GOCATTTCCC TTTGGTGCTG CGTTTGCAGC	300
55		

	CTICAAGIAC CACACGAIGG ATTICTCAGG GCTATACGGC AAGTGTAATT CAGOGTACTC	360
5	GTAGCAGTIGT CCCAGCTTCC ACTGAGCAAG CGGATAATTA AATTTAATGG CACATCTGAT	420
	GTAAAGGTCT AGAGCCTTTA GGGTATCTTG TGGAACGTGC TGCAACTTGA CAGCCTGCTG	480
10	CASCITUTGGA TOCAAACAAT CAAATTCATA GATCTITUGG AGTTGGTATA ACOCCTOOGG	54 0
	AGAGACOGIC TIGICGIGIG CAGCAGCCCG CTCGAACCAT CGTATAGCAG AAATGACATC	600
15	CIGITCAACA ATAATTICAC CIGIGICATC ATCCACCAGG CCATTCAGIT GOGAACATAC	660
	CCAACTTATA CATOCTACTG CTCTGTCCCG AAGA	694
20	(2) INFORMATION FOR SEQ ID NO:1103:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 674 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1673RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1103:	
	GATOCCAGOT CITACOCTOG CICAATTGAA AACCTITICT ACACTAGOTT TOTTATCAAG	60
45	GAAGGACGGC TAGTCCTAGA AGATGACGAT GAGGGCTTCC CGGCCATCCG ACCCAAGGAA	120
	CCCCTCCCCC AGGATCCCGC CGAAAAGGAA CTGGAACGGC AGCGACGGAA TGACGCGGC	180
50	CAGAAGCATA TCATCTTCCA AATGGACATG GCCACGTGGA GGAAGCTTAT AGACAAGTTC	240
	CACATCACAG AGTCATTTTT ACCGTGATCA TGTATAAATA GCGCGCATCT ACGTATCACC	300
55	COCTOCCOCO GOOCTCACCO AACCAGOCAC TGCTAGCAGC TCATCTATCG CCCACTTCGC	360

	MIGGICAGE GEOGRAPEST CIGIGICAE GEOGRAPA CEL GENEGO CONTRA	420
5	CCACCCGATC ATCACCGCAT TOTCTGTACA TAGATCTGGA OCTGGATAGT GAAAGGAGTC	480
	CAACGETCTG AATAGITCAG TCICGAGICT GGCACGCAGG CGCCGGTTGG CGCATACGCC	540
10	GCCGGAACAC ACAAACTGTG CCACATCAGC AACCTTATCA GCATTTGAGC CGCAGCACCA	600
	GGITAATCIT GGTAATCAAA TGGICGAAAT ATGGCCICCT GAATCIGAAW TGCTGCIACC	660
15	assastras acta	674
	(2) INFORMATION FOR SEQ ID NO:1104:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 726 base pairs (B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
25	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: INA (genomic) (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1673UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1104:	
40	GATOGOTOTA COGACGITACT GCATGOCTGT CITOGTCTTA AGITTAAAAAC CACAGCACOC	60
	AATOGTTTAC ACCGCAATCT TAGACCAGGA GCTAGTGCTT GCCAGCCCCT GTCGTTCAAA	120
45	TGGCAGGACT GITGITTGGT TGTGAACCTC GCGCACTGAG GAAAGCGGGC GGAAGATCTA	180
	TTTTGCACCT ATTCGCAACC GTTTAGATAT TGAAAGCAGG GCAACACTAG TAAAACTCGA	240
50	AATTAGGACA TIOGIGAACA GAIGIGAGCA GAGGATICOG GATGOOCIIC GAAATGATGA	300
	GOCCICATOC TOCATACCCT GOCCGTOCOG CGTAGTGTAG ACCGTOCAGC GCATOCTGCA	360
55	AAACAACGOC GCCGTGGCGT CGGCATGCAG GTAGCACAGC ACCTGCAGCA GCGCAGGCGT	420

	OCATOCAAGA GTAACOCCAC ATGICOGOGG CGIIGCTCCG TAIGIACAAG TIAIGICATT	480
5	ATTICIACAG ATATCATGIT GAATATTAGC CCGCGATCAT CTACTCAATG GTATCGTTTG	540
	GICTATCTCG CTTACGTCAA GATGCAGGCT CCGCCCGGGG ACTACGCGCC AGGGTGCGCA	600
10	GACCAGTITIG GTATAGGAGA AGCATGATAC TOCTITIGGAT GCTGGTCCAG ATGAACCTIGG	660
	GGCCCACACC GCTGAAGGCG CCACCCAGTC CCTCGTIAGGG AAGTIACGACT AACAAGCTGC	720
15	OCENACEA	726
	(2) INFORMATION FOR SEQ ID NO:1105:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 657 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1674RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1105:	
40	GATCTCATTG AGGTACACAG ACACAGCTGG CAGCCACGCC CACGCCTGGA TGGACGAGTT	60
	GOCCAAGCAA TCATTCCGGT TGTTTGCCAG CCCTGTCGTG TGTTTGTCTT TCCTCGTGCA	120
45	CCTCTCGAAC ATACCAGAAC TACCAGGGGA ATAGCCACGI GIAGATOGIC GGACCTAAGA	180
	TATAGTATCA AAGTOCAAGT GTGCCACAAA GAAGAAGTCT TTGTGGTATG TTGTCCGTTC	240
50	CGTAGAGAAA GCTTCCGACC TTATTAATAG AGAGTGTACC GTCGTAAACA GAAGAGGGT	300
	ATGICACCCT GTGCAGCATG TAGATGGACT TGGGTATCTA GTCAGCCGTT GTGCTTGAAG	360
55	GIGGACCAAA CTAATOCTTA GIGCATAGIA TITIATGIGGG GCGCCCTTIG AACCAGCCTT	420

	TIGGAIGUI CGAAGGCCA ATAATACICC ACGIGACAAT AATATACGIC AACTATTAAC	480
5	GOCTAAATTA TOOCTTOOGA GGAGAACATO COGTTAATTA CAATTATCAT TOTATATTAT	540
	AAACATATTA TAAAACGTCC ATCTTGCTAA TATAAAAACA ATCTAGGTCG GCTTACCAAC	600
10	CATALTACAT CAGTAGGCAG GGGGATCTGC ATCCGGTCATG GCGTGGAGTA TCCAGTT	657
	(2) INFORMATION FOR SEQ ID NO:1106:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 695 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
25	(ad) CONTORDE CONTORD	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1674UP	
	(A) CREANISM: PAGIO740P	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1106:	
35	GATCATCATC AACTATATOG AGAAGGAGTG TGACOGOGGC GITGCTATGG GTAAATACOC	60
	GICTACCCTT CACCGGCAAG CGGTCCGAAA GCTGGTGGCA AAAGATTTGG AGAACTTCGG	120
40	OGTAACCAAC AGCCTCACGC TGAACAGTCT CTCCCTATAC TTTCGCAACC TAACACGGGA	180
	OCAGOGOGAA ATATOCATAT ACAACAACTT CACOCACTOG AGCTTOCTAA TOCTTOCOGA	240
45	AGAGGACAAA ACCAAGTACT GCAAAAGAAA GCAGGGTTCT TOGTCAGAAT AACAGTAATT	300
	GEAACTATAT AATCIGGAGC TICTCCCAGC GGEAGAAGGT CCCAATTIGT AATGEACTAC	360
	diram income network continue and and	500
50	TACCTGAGCA CTTGTGTCCG CCTCATCGCT CCTTAGAAAC TCGTGTTCAA GAGCTCGGAT	420
	GCCATCTGAC ACAAAGGTTG CAGACGCAGG AGAGTATATIC TOCAAAGCCT TGGGTTAACT	480
55	TICTAACCTA ATAITTIGCA AATAAAGCOG AGICGCAGIG TAICACTGCT CCAGICAGIA	540

	GATEGORET TEGHAMATA TETETTETAT GOSTOGAMEA TITTAAGICA TAGTITIGET	600
5	TITICCCCIG ATATACTTCC AAATACATAT ATCACIGAAG TICCATOGGA AGCACCTCCA	660
	CAGTACGECC TAAGAAGAGC AGAATAATTG CTCCA	695
10	(2) INFORMATION FOR SEQ ID NO:1107:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 654 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1675RP	
25	(A) UNGANISM: PAGIO/SKP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1107:	
	CATCOGIGCA ATAAACOGCT TGAATGCACT GIGGAAGTAG TIGCGGGTCT CCATATCAAA	60
35	GICGACAAAG AATATCTOCA GETTETTACE CAAAATGTCA AGCACATATC CACOCACTGG	120
	ACCCEACCOC TTATCOCACT AAGITACCAC TTCAAATCCA CCCAOCTTGT ACTTGTCCAT	180
40	TOGCAGAAGG CTTTOCAAGG TOGACAGCAT GATCAGCTTG TCTTOGTGGA AGGGCTCCTC	240
	CTCTATCCCC AGCTCCTGGC CAATTTTGAG AAGCGGTAGA AGGAGAGCAG GGTGCCCCTG	300
45	CATGITOCOC AAGATAAACA GATOGAAGAC CTTOGOCOGA ACOGTOCGAA AGAGOGOCTC	360
	CAGCACGIAT AGTIGCACTC GTITCGCGCA GGIGCCCTCA AGAAGATGCT GAACCACCIG	420
50	CTOCTCCCAC AACTGCAGCC ACATCTCCAG TITATCCTCT GTATAGTGTC GCACATATAT	480
	ATTOCCCAGE AAACTOGTCA CACTETTOCE AACCGCOGTE GCAAGAGAGT COCACCACAT	540
55	CTATCCCAGA CCOGTCCCAA TGAACTCCGG CCCCACCTCT AGAACAATTC CCAGGTCAAT	600

	CCGCTCCGAT AGCACGTCCA CCATGAAGTA CACGAACCTC TITGAAGGAC TCAG	654
5	(2) INFORMATION FOR SEQ ID NO:1108:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1675UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1108:	
	GENTCOGCTT CCACACCGAA ANCGCAGAGG ACCAGGACGG TGTCTCGAAT GTCGTTGGCG	60
30	ACGCCATCAC GCACGTCAAC ACGCTCTTTG GCCACAACGG CATTCACGCC TACGTTCATA	120
	AGAACATOGT GITOGTOCAG CAGTOOGGOC TGTOOGTGCA GGOOCTCAGG TTOCTGCTCA	180
35	ACCACTACAA CTOGGTOGAC GACACOCCTG GCTOCACCCC CGGGCACTCC CGGGCTGTCT	240
	COCCCGTCAT GACCCCGGTC AATTCCTCGC TGGCCATGTC TOCAAGCACC GCCGCATCTA	300
40	AAACCCCCTC GGCCGCGACC GCAACAGCCA GCTACTTTAG CAATGGCCGT TCCACCAGTC	360
	SCGICCAGIT TGICTGIGIC ACTGGGACTT CATCGCCGGT CCTGGAGCGG CTGTTCCAGT	420
45	CTATCAATGA ACTGGCCAAA AAGGCCCACC TGCCCTACGG ATACACTGTC GCCTAGGGCG	480
	ACCCTATTAC CACATACCCT AAAGAGCACG TOGAAGGITC CAACGAATTA TITGGCATTC	540
50	TAGACAAACT GAACTICATT GOOTGCTGAG COCCCCTGTT ACATAGGTTA TTAATCAATT	600
	AAATCCTTIC TCTGGAACCT TATAGAGCCC TGCACCTTGC GCTGCGGACG CATATCCTTG	660
55	CTGACTAGTT GTCACCCGTA CCCTTTAATA AATTACGTAA TATGTOGTAT TATCA	715

(2) INFORMATION FOR SEQ ID NO:1109:

	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 568 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1676RP	
20		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1109:	
	CATOCOGACA CCAGCATIGOS CTOGITOGAAC GOGITOGAAGI CTIGTIGTOCAG CACCTIGTIGOC	60
25	The second secon	00
20	GTGTGCCCCC GCAACACAGG AATTTGGTCT GGCGCCTTGC CCACCTCCTC CACCGGCACT	120
		120
	ACCECCAACG CCCCTCCCCC CCACCAATTC CACGTAACCG AAATGAACTT GCCGTTAGTC	180
30		100
	TICATCACAT TOGAATCOCA ACCATTGATT GICACITICA GGITCTOGTA GAAGAGITCC	240
		440
	TICTITIGITG ATTIGICOGAA GACGIGICIA TACTIGGAAG CCCCCACAAA CTTCCCACTG	300
35		200
	CAGTOCOGIT AGITTGCCCFI COGCACAAAG TOCAGTOCTG GAGAGTATGA CATACCTCAT	360
	CCTTGCAATT CTTTGGGGTT TAGCAGCTCT ATATGGGTGT ACACGGTAAA CATGGGTAAC	420
40		
	TAAATATGTA ACGIOGAACT GAAGGGTACT GGAATCIAAA GCCGAAAGAA GIACCCGITG	480
	ATGGTGATGG TACTGTCAAG ATGGCTAAAG CGAACCTCTG GCCTGGTTGG AACTCACAAA	540
45		
	GGTCACCAGA CTCTTCTTAT TCTTGTTT	568
	(2) INFORMATION FOR SEQ ID NO:1110:	
50		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 568 base pairs	
6.5	(B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single	

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1676UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1110:	
15	CATCOCCOCC CICCHOCCTC OCCTGIATTA CTACOCCACG AAGCAATTIGT ATAACCCACA	60
	TATTGTAACG TTTGTACTAT CCTCCATGGC CTCGCCCACC CCACACGCCG CCTTTCCTCC	120
20	ATTCGCCTGC CGCCTTTCAA CCTCGCCCA TGGCTCGCCC ATTAGCTGCC	180
	AGTAGOGATG CAACOOGAAT GOOGAAGATG GAGCOOGCAT TOGTGOGTAC CAAAAAACCTT	240
25	TITACOCCIA CIGITIOCIG GICTAACOCA TOCACOCCAC GACOCIAACO AGIATGAATA	300
	COGACCTOTT TROSCAGOTO GTACTTOTOC CGATOCTOCG GTOCCOCATA GOGITTTIGTG	360
30	TECTICIAIC ACCEIATOCA ATGITATEAT COGTETICO COCAACATET WCTAACACCE	420
35	GACAGOGIGO TOGATACISCO GIGOCOSCOG CIGGCAGCOG CACTIGACIGAT GIACACAGIA	480
35	GITGTGAATG CGTGCCTAAG CGCCAACCGG CGCGCCAAGC TGGCAGGCCG TGGACGCCAC	540
40	TOGAGCAGAT GCCCCACCCC ACTTGCCT	568
••	(2) INFORMATION FOR SEQ ID NO:1111:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 653 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
~~	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE:	
5 5	(A) ORGANISM: PAG1677RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1111:	
CATCIOCAAT TAGOCCATAT AAACIGIOGG TACTGIGICA TCACTAGIOG GCGTATGCAC	

60 TOGTAGIOCC AACTATOCGA ACAAGGGGAT ATGAAGATGG CCTGGCAGGG CTTAATTITA 120 CATAGGCAGA TIGAGCAATC TICCTCCTCA AGGCCTGCCG TIAGCTTTIG TAGGTTCCGT 180 ACCOSSICTA GIGCCICITT GITGAACGCG TIGGCCCCTIC GCTTCCACGA TITIGITICAAC 240 TOGACTOTCA TITTGACGCA TOTATATATO TOCTOTIGIOC COCCACGGAA ATCCATTICCO 300 ACCTOCAATA TGTCGCCGTC TTTCAAGGGG TAGTCTTTCG ACATAACCGA TGCCTGTGCA 360 ACCOCCATCT GATTAACGAA CCTGCCCCAC CAGGACTTGA CCTCCCCCAC ATTACCAATTG 420 CCCTGCTCAT CCACCITAAA CACCCCGTGT GTGCGCCCACA CAACCTTGCT CTTGAATACC 480 ACCCCCTCCC GAACCCCTTCC TGTGTAACCC 540 COCATAACCA ACTOCGASCT GEGGCCTGCC GTCCCCACGA TGGGATCAAA AAAGAGCCCC 600 CCATTATTOG TOGTCGAGTG GICAATGAAC GCCGTTAACC GCAGCGAGAA GAA 653

(2) INFORMATION FOR SEQ ID NO:1112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 625 base pairs

(B) TYPE: mucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1677UP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1112:

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	CARCINISCE TRANSCUCT CUCCOCCION CONTROPAS CONTRAATON ACTOMICOS	60
5	CGTCGGCTAC ATCCCAGAGC ACTTCAGGGC GCGGCTGCTG TTTGGGCAGA CGCTGGGCTT	120
	CTTTOCCCAG COCCCCCTCA CCCCCAACCT CCTCCCCTTC CCTACCCCCT CTCCCCCACCT	180
10	CATCCAGOGE CTCGACGCG GCGAGCTCGA CCTCGGCGCTC GGCCTCACCG AGGCGTTCGT	240
	GCGCGGCATC GCAGACACGC CAGCCGGCGC CGCGCCGCGC	300
15	CGTGCGCTCG CCACTCAACT GGGCGGTCTC GGTGGGCGCC GGGTGGCGCC TGGAGCACGT	360
	GEACCACCTG GACCICCC GOSTOCICCT GTCACCCCTC GCCACCCCCT CCTACCTCAT	420
20	CASCILATORIC CIUDOCURIO: AGOSCOGOCIT COSCOSOCOC TITROCOGOGO: AICCOGRIGIG	480
	CCACACCTTT GCCGGCCTGC GCGGCGCGT CAACGAACGG CGCCGGGAC GCTTTCCTGT	540
25	SOCACCACTT TACCTCCAAC COCTACCACG ACGCGGGGGA CATCCGCCTG CTGCGCCAACA	600
	TOCCCACOCC CTGSCCCTGG TGGGT	625
30	(2) INFORMATION FOR SEQ ID NO:1113:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGIH: 643 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(VI) ORIGINAL SCORCE: (A) ORGANISM: PAG1678RP	
45	(A) ORDERISM: PASIOTORP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1113:	
	GATCCOCTGT COCCATCATC OGAGACATOG CCTCCATGTT CCCCGATGGT AGGATAAAGC	60
55	AATTGTACOC CCAGACTTGG GTCACAGAGT TTATCAAGAA AACAAGAAGT AACCCCAACT	120

	THOTCHOC MCIMBONT MCIOCINENT GOOCHEMEN HENGENAME CHICAMETAN	100
5	CCCTATAGCC TEACACTCCA GAATAATFEA TCTEATEACT CASTITUCIEC TGCGTTAGCT	240
	COCTOTOCIC CIGITATICT AFAATACTIC COCTGCATTG TCTTCATTAT TGTGTCTGCC	300
10	TODOSACAGA CODETTOGIT GICTETTETT TIGITOGACE CIGCACTGAC CTGGGCCATGC	360
	TOCTOTTICT AGROGITIOG TACAGGITIOC GOGICTITIT ACACAACTIT TOTACTAGGI	420
15	CTICIATCIA ATCCCATCIA CITTICIACT TICCICICET ACTITATCOS TOSCACOOSC	480
	TOCTOGICTE ACGIOGCAGO TIGIAGCATO TATATAATIG TATATATOGE OGTOGCAACE	540
20	ATCTACGOCT GCTATACATC TGCTGCCCGG TCTGATGGGC CGAGCCGTTC ACCAATGCAG	600
	TAAAACCACA TAAACITTTA AGAGITACAA OCICAAAAAC GIT	643
25	(2) INFORMATION FOR SEQ ID NO:1114:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 721 base pairs	
30	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1678UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1114:	
	GATCOSSETT CEASTCOSSE GASSSSCTEC ASCISCACCAS COCTTETTTT TOSCOCTOST	60
50	AGICGAGGAT TGITGACTGC TAAACCCATA CAACCACATA TTGCACTGGT GGCTTGCCCG	120
	OTTAGOCOGO OCTOGOSCTO: OCCOSTTAGOC OCCOSCOGG ACCCACGOZA CGACACGCTG	180
55	CRIRCOCCIC ACRICCATCA CCARCURCAG COCCTICARC GTAGGCCGGA CARCTICAAAA	240

	GTTACTACAA TTTGAGGTCT COCATACTGA CACAGAGGGT CTTACACAGC ACCAGAGGAA	300
5	TOAGCAATGG CTAAGCAATC TCTAGGTATG TGACAGAACG ATGGTGGCTC CGAAACATTG	360
	GGAATGAGGG TCTCTGGCGC TGGGATCCGT GGTAACCTGG GCATACGGCC CAGCGCCCAG	420
10	GOGGACCTAG CATAATCCAG TOCGTGGAAC AAGITGGTGG CCCGGCACAG TACTAACATG	480
	TOTOCAGACO TITTOCTOCCA CAGAAGAAAG GOCAGAAAGO COTACTTOAA COCCCCATOT	540
15	TOCCAGOGOC GOGICATCAT GICTOCTOCT CTATCCAAGG AGTICAGAGA GCAGTACAAC	600
	ATCAAGTCTC TACCAATCAG AAAGGACAAC GAGATTATGG TTGTGCGTGG CTCCAAGAAG	660
20	GOCCAAGAGG GCAAGGITCT TCTGTCTACA GATTGAAGTA CGCTGTCCGC GTCCACAAGG	720
	G	721
25	(2) INFORMATION FOR SEQ ID NO:1115:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 633 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(b) totolkar. Make	
3 5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1180RP	
45	(xi) SEQUENCE DESCRIPTION: SEQ 10 NO:1115:	
	CATCOGTCTG ACGGTGGTCG AGTTCTGGAC AAACGCCGTG CTCTTTGACG AGATCGTGCA	60
50	GCCACTGGGC GAGATCATCG ACCTCTACAC CCAGTTCAGC GGCGTCCACG AGATAGACCG	120
	COCCIGIOSCO ANCACALTITO ACCACOCCAG OCAGGIATITI TIGICOCCOG CCATGATIAA	180
55	CGAGAACAGC ATACTGATTG GCCACGGCCT GGAAAAACGAC CTGAACGTAT TACCGCATTAT	240

	ACATGATAAA ATTATIGATA CAGCTATATT ATACCCGAAT GETAAGITCA AGTCCTCCCT	300
5	COGGAATCTA GOCTITICAGG AGCTCAGTAG ACGGATCCAG ACGGGCAGC ACGACAGCTC	360
	AGAGGACGOC ATTGCAGCAA TGGACGTCGT CAAGCATAAG CTGGGCATCC CGCTCGACGG	420
10	CAAGACGIGG TAGCCCTACG GCTGCTCCTC CAGCCGCGTG AGCCTGTCTT CAAGCTGGTC	480
	CIGOCICICA ATTACOGIGI GIATAACCIG CITAACCICA TOCCCATCAT	540
15	CCTATCTTCT GGAAGCIGGA ACTIGACGTT CCTGCTGCGG GTCACGATCT GGCTCTTGCC	600
	CACCITOTAC CICGATCCCI CCGGAATTIT GCC	633
20	(2) INFORMATION FOR SEQ ID NO:1116:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	· · · · · · · · · · · · · · · · · · ·	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1680UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1116:	
40	(AL) SEQUENCE DESCRIPTION: SEQ ID NO: 1116:	
	GATCOCCCC COCCETOCCC COCCATTTCCC CAACCCCCAC COCCACCACCAC CTCCCCCCATT	60
45	CGAATOGCAT ACGICTICGC CACGCCGGAA AAAAAATTIT CGGCTATATA AGGAGAGGCG	120
	GCGGICTTGC TGCAGGCAGT TTCACTTTCT CTAAAACCAA AGAACATGGA TTTCTTTAGT	180
50	CACTOGETTE CITTACACOGA AATOCAATTE TOCACOGTOG CITTOCATOGE AGCOGETGOE	240
	CCCUTCOCCT COCCTCACGC CAACCTICACC ACCOCCACCG CCAACCAAAA CCAACCAACC	300
55	TIGGICACCA TCACCCACTG TGAGGACAAG ACCOCATGCA CTGCGCACGT CTCTCCAGCT	360

	THESICION COSCINCOT CACCATONIC AND TIGIDA COTTONICA CACCIONICO	420
5	CCACTATOCA CCACTGAGGC TOCTAAGCCA CCAGTITOCA COGOCAAGCC ACCTGCTTCC	480
	TOCAMORGA CTGTTCCTCC AACTGAGACC CAGTOGTCTC CTCCTTCACT GGTGCCCCTG	540
10	CCAAGGCCCT ACCAGCTOCT GGTGCCTTGT TCGCGGGGCGC TGCTGCTTTG TTGTTGTAAG	600
	TITAGITICOG COGOGIGAGO COTOGITTOG TITAGAGATA TATAGGAACT TATGIGACTG	660
15	ATTCTAAGCT TITTACACCAG CATGATTTGG TTCTGCGGGG CACCGA	706
	(2) INFORMATION FOR SEQ ID NO:1117:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 696 base pairs	
	(B) TYPE: nucleic acid	
a.c	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
3 <i>0</i>	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1681RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ 1D NO:1117:	
10	GATCATTCTA AACAGATTAA OCTTOCTOCA AATTACTTTA TYTOCTTAAT CTOOCATAAA	60
	TOGTTACATT COGACAATAA COTCCCCGTG GTCCTTACAG ATATACATCT ACCGACAAAA	120
15	TTICOGOCAC ACACTOGIAT AGAAGAAAGA AATTIGATIG AAACTICIGA GCTAGATOOG	180
	ACCITICACIG GACTUTICCC ATTIAACCIT TICAACAAAT TOCAAACICA TGIGITUAAT	240
50	GCCTTGTACC ATACCCATGA AAATGTATTT ATTGGAGCTT GTAAGGGCTC GGGTAAAACT	300
	OCANTOCCAG ANTINOCTIT ATTENGTOAC TOGAGAGATE GTANCOCACG TOCCGTCTAT	360
55	ATATGTCCAT CTCAGCAGAA AATTGATTTT CTGGTGAAGG ATTGGCGAAA CAGATTTTTA	420

	ARIGIGOLAG GIGGAAAGGI TATTAATAAA CICACATTGG AATTAACTAA CAATCITCGA	480
5	ACCCTAGCCC AGTCGCATTT AATCTTAGCG ACCCAGAGCA GITTGACCTG CTTTCTCGTC	540
	OCTOGRARAG AGRARARAC ATCCAGROAT TAGROCTIGHT GATTICTAGAT GATCTTCATA	600
10	TGATCAGTAG TGACTTGCCT GGCGCAAGGT ATGAAAATAT AATATCCAGA ATGCTGTTCA	660
	TICOGOGICA ACTICAAAAC GOCCTICOGT ATAGIC	696
15	(2) INFORMATION FOR SEQ ID NO:1118:	
	(i) SEQUENCE CHARACTERISTICS;	
	(A) LENGTH: 659 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1681UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1118:	
	GATCAGGAAT GATCCCTCAA TIGICAGGAA TTATGGTTCC ATATTGGTTG AAITTGCCAA	60
40	GATTACTCCT GATGGTATOG TANTGTTCTT CCCCTCATAT TTATATATGG AATCCATTAT	120
	TICAACTIGG CAGACAAIGG GGATICIAGA CGAGGITIGG AAATACAAGC TCATCCICGI	180
4 5	GGAAACACCA GACGCACAGG AAACTICICT AGCTTTAGAG ACTTACOGAA AGGCCTGCTC	240
	GAATGGGCCC GOCCCAATAT TACTTTCTGT GCCCCGTGGG AAGATTTCTG AGGGAATTGA	300
50	TTTTGACCAC CATTACOGIA GGACTGIATT GATGATTGGA ATTCCTTTCC AGIACACTGA	360
	ATCGCGTATT CTAAACGCCA GGTTAGAGTT CCTAAGAGAA AACTATCAGA TACGGGAAAA	420
55	TGACTITITA TOCTITGATG CAATGAGACA CGCCGCTCAA TGTTTGGGAA GAGTCTTGAG	480

	COSTANDATI CATTATOCCO TOATOCTOCT COCCONTCOC CONTCTCARS ANALAMANE	540
5	CAACTTCCAA AATGGATCCC ACAAGCCCIC TCTGATGCTG ACCTGAACCT TTCTACTGAT	600
	ATGGCGATAG CTAATACAAA ACAATTCCTA AGGACGATGG CACAAGCAAC TGATCCGAA	659
10	(2) INFORMATION FOR SEQ ID NO:1119:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 707 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1682RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1119:	
	GATOGIAAAA TITIGCIATAC AATGGITTIGG GIAGGICCTT TAAAAAGGICG TCAATCTCAT	60
35	AGTCCCTCAC ATCAAGCCGA ATGITTAAAA AACCCACTCT CTGATGTGTA GCCCGAGCAG	120
	GCCTTGCGTC TCGCCCGGTCC CTGAAACGTG AGCGGCCGCA GGGGCCCGTAC TCTCGCCGCCC	180
40	CATACGIGCT TICCCCCAGA COCATGOGIG AAGCTAGICC ATTACGTAAG TCTCCCACGGC	240
	GATATTOCTA TAATAACAAT GTAATCGTTA ATACTCACOC TCAAGTAACC TTGCGGTGGG	300
45	TCATGTATCA CITACOGTAG TAGTGCCGTG TGTCTTTTTG CCGTTAGTAT CCGATGAAGT	360
	TTOSTATOGA OGAGAAAAAG ATGITCATAC TTTCTCACCA GTACCCTOGT TCAAGTGTTC	420
50	GTCAACAGAC ATTGTCCCTT CCAAACTATC CTGTTTGAAG GGCAAAGGCT GTGTGTCAAG	480
	AACGAAGTIT TCACCATITT TCCGGAAGGC TCGGGACAGC GATCGAAAGA AATAGGATAT	540
55	ATACGIACAC CITICITIAA ATATCATITA AAATATOOTG GAATITOGAT ATGTGGCCAT	600

	ACTOSCICTT CASCITCCTT ATCCATCAGA TAGAAGGAGC AAACTGTOCG AAGGTGCCTT	660
5	CCACAGITAC TTAAGITICC GTAAGCAACA AGGAGICTGT ATGCCGC	707
	(2) INFORMATION FOR SEQ ID NO:1120:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 700 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1682UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1120:	
	GATCCAGTGT GTACGCCCAG AGTCCCCCTG GCCCACCAGC AGTACCTGCT CCGTCTCGTT	60
30		
	GAAGITCOCA ACATTOCCGT COGCATCAGC ACCCCCCTG AAGIATCTTG TACCCCCCCT	120
		1.00
35	GAATCTOCTC 000000TGA TCAGACOCAC ACTAACTOOC GTACTCTOCA ACACAGTOTC	180
	TACCACTITIC ACGUACOCGU ACATUAGOGG CAGAACGAAC TOGUUGOCCA GAGOGUUTUC	240
	INCIALITIO ACGIASCOSI AMITACOS CASACIANO TOSTOCOCA CASCOTTA	210
	CTCCCCCAGG TTTCCCAGCG GCTCTGTGCC ATAGTAGTTC CAGAAGAACC GCGTGTCTCC	300
40		
	ACTICOCCAC CACCCTICCC CCAACCCTTC GTTCCCCTCC ACACACTCCG TCAACTCATA	360
45	OGIGIACEAA TAGIACAECG TIGOCTIOGC GAGGIGGICG CSCAGIAGCG CAACATACIG	420
	GITGTOCTICT GCACATGGCC GGATACTGGT GITGACCAGC ACCAAAGAGT GCGCCGTCAC	480
50	TITIGAAAACA GAATGOOCAC CCAGGITITOC CACCACCTOC ACGCGGTCCG CCGTTAGCAC	540
	CACGCGACTA TROCGCAAAT GTAATATCCC GATCAGGCCT GCGATCTTGC GAGTTTCTCC	600
	ARCHITETTA CONT. A BARTESCANCE. CONTENTE CONTENTE CONTENTE CONTENTE CA BRITANTO CONTENTA CA BRITANTO CONTENTA CA	<i></i>
55	ATCTITAGGG AAATTGCTGG GGTCTAGGAG TGTCACGCCC GAATGGTGAT GOGAGATAGA	660

	CAACACCOCT TCACTCTGGG AAGTATTAGA TGGCTTGAAA	700
5	(2) INFORMATION FOR SEQ ID NO:1121:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 652 base pairs	
10	(B) TYPE: mucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
0.0	(A) ORGANISM: PAG1683RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1121:	
	GATCIATATC ACCAATCATC ATGGTTTTGA AACATTGGGT GCTTAAAAAAG GGACACAGCA	60
30	AACTACAAGC AGGCAGCACG AAGCACTICTG CAGACTAAGG GCAGGCCTCA TCATAAGATG	120
	CTPACCOURG ACCTAGRAAA TOCCATTCOG TOCCAACGRG CTCAGRGRG COCRGROCIT	180
35	GATGOCCTTC GACAACTTGT GGTGGTGCCA AATAATAGCG ACTTCTTGGT GTACTCCAGT	240
	ATGGACGAGA GAGGCCTGCG TCTAGTTCAG ACATATACAG AATTGCTTGG CCCGAATTAT	300
40	OSTISTAGAAG AGCTIGCTISTA CTCCGAACGG CTGCGGACAA TATTCGTCCG CACGACCAAG	360
	TOCTUACTOC TACTICATIC GAGCAACITA CAACATTAGG ACAAGATAGT TGACAAAGGA	4 20
45	GOCATIGACO ATGOCTIGOCT GITTICAACAT OCATGTIGOGA AGOCTICACAC GTIGGATIGACG	480
	GIGCITGITT ACTOGRICAC ASSGRICGAGC AAGATAAAGA TGCTGACATG GGTGGGGGGG	540
50	CAGTICCAAG COGTOCATGA GGTCOCACTA GGCACGCGAT COGAAGTCAT CCAGCTCAGT	600
	AAGTGGGGGC CCGCATGCTG TGTGGTTGCT TACCTCCGAC GACTGTATAC CA	652
55	(2) INFORMATION FOR SEQ ID NO:1122:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 718 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1683UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1122:	
	GATCTOGTCA AATTCTGCTC TAGCATTATC AACTTTGTGA CCACAACTTA GAATTCCCCC	60
25	ATCATOCATT ATGITTATAG ATGIACAGIT CTAAAAAATT COGTAATATA ATGAGACCTA	120
	TCTCTTTTC TCATCCTPAT AGTCACCCAA AGTTTAACA TGTGACATGC TGCCAGATTT	180
30	ACAGICATOT GOOGCTATGA TTTCTTGCAG AGACCTGCCA CAATTATAAT GTGTTAATAT	240
	ATTOCTTOCT CTGAGGITGA AGAGOGAGAA AAGTTCACTG CTCCCTAATG TTAAATTCTT	300
35	CTOOCAAACG TAOCAOCGGT TATCTTCATC TACCACCAAA AATTCAGATA TGATCTGGGA	360
	TAACOCATAG GIOCTICOCA TCACGITCAC TTTCAAAAGA TIGITCIGIA TACCCCATIG	420
40	GETTETTE ATGGACOCAC TETTAATOOF TOTACTTAGG AATTOGTTAA GOGTGETTAT	480
	COGARTATIG COCCOCAGIT TCTCAAACAA TGTTATCOCA TCTAGCTTCG AACCATTCTC	540
45	TAGCAGAAAC AGATGAAOGT TICTICCATCC GCTAAATTICT ACCTTOGCAA GCAGCTTTTIC	600
	AAACAAGTIC ATGAGAGCIG CIGIGOCIGC ATTITTIGITT GIGOCATAGA GCTCATTACA	660
50	ATATAGAGAA GCTTGGTTAT AATTCCCTAG ATCATCAACT AGGATCCCTA ACGCTGTT	718
	(2) INFORMATION FOR SEQ ID NO:1123:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGIH: 577 base pairs

	(B) TYPE: nucleic acid	
_	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1684RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1123:	
20	GATCIGIACA CITCAATATC GAACCAAGTG TCACCCCAT ATTCTGCAGA GATTTGAAAA	60
	ACCCACCAAA CCAATATCAC ATCACCCTAG ACCTTCCACC CACTAATCTC CCCTCATTCC	120
25	TOGATOTOCT TTAACCAAGO AGCAAACOGT GTOTCATGTT GOTTTTCCCCA GOTAATAATO	180
	TCATGCACCA CAGCCATAGA TTCAGCATAA TGAAGGIRIG TTGCGCGCGC CTCATTACAC	240
30	CATTIGATAT ATATTTICCC CACGOCATOG ATGAACTTCC CTTTCGTCTG CAGCTTCCCA	300
	AAAATAGGTG TCAAAAAGCAG TTCCTTGTGC AAGTCAATCA GCCCATAAAA GATGTCAAAG	360
35	CCAACACACGO CCAAGITITIC GICCGIGGGC ACCAACGCCG GCCACAAITIC TGCCCCGIAG	420
	ATTICTACOG CAGCATOGOC CAGGITCAGA CTITICICIT CGAGCACAAT AAGGICAAAT	480
~ 0	ATGIAGCICT GOCGCITTAC TICICIAGGA TIAATCICIG AAAGCTOCTC GTOCGICAGT	540
	TTOCAGIACT COGTOCAAAG TOOCACOGGG COGCTGA	577
45	(2) INFORMATION FOR SEQ ID NO:1124:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 707 base pairs (B) TYPE: mucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(D) TOCOLOGI. IMPAGE	
55	(ii) MOLECULE TYPE: UNA (genomic)	

(vi)	ORIGINAL	SOURCE:
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(A) ORGANISM: PAG1684UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1124:

CATOCATCAC CACCAGCTGG ACCTOGTCGC CCCTCTGGGC CTGGCGCCAG AGAACAAGGA

AACOCTOCAG AACCTCCCGC TCGCCCCGCT CAGCGTCACG TTCAAGGACG TGGTGACGGA

CTACTOCCAG GCCCACGGCC TOCTOCTOCA AAAGACGGGC GACGTCGCCA CCCTCCGGGT

CTACCAGCAT GCACGTACTG TCCCGGTCTT CACCGTCACA CACGTACACC GCCGCCGGGG

TGINGCTCTG TGCGAGGACG TGCTTTGGGT TCAGGAAGGG ATAGGCTTCA AACCTAGGTA

CTTATACGAA CTAGAAACTC TTCTAAAGAG CGCTTAGTCG TCTCATATAT ACAGGACCTA

GRACICITEG COCACICACT GECCCICETC GCITTTOSCG CICICGSCCG CGGCCICCGT

CTGGGGCAGG GCCTGCTCCT CGCTCTCCAG CTGCTCCGGG TAGTGCTCGG GGTGCTGCCG

GAACCATCCT GCATCACCIG GAATTCTCCA CGCAGICAAT COCCTTAGGC TOGGCCTCTG

ACTIACACGAA GCACGOGAAC GCAGOCTTGA ACTOCTOGOC GCACGOCCOG TGCGCCATGC

COCCASCA TOGGCAGTOC CAGTIGATOT COCCOGNIGIO GESATIGNAT OCICCIOCIG

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(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:1125:

(A) LENGTH: 666 base pairs

COCTGOGGAG COTCACCOGC GOTAGOTTTG TOCTCOGGGG CGCTGGG

(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ENA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1685RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1125:	
10	GATCAACTIC GOCTAATCCC TIAATCATTG TCACTGCTAA CTTGAACTTA GICIGIGIGI	60
	ATOCCTATAG TGAACGITTIA ATGTGATGGT TTTATAGTAA TCCATGGAAC TTTATCCGCG	120
15	AACCCTCAAG CTGATCATCA CGTGAGTAAC CGTCGATATG CAGAACAGAG GATACCATAA	180
	ATTOCIATTA GIAATCAATT AATAGACTIA CATATAGCIC AAAGCIGATC ATTGATOCGT	240
20	CTCAAACTCT TTTCATCGTC TGAACCTTTC GGATTTTCAC TTCCTGTATC ATTATACCAT	300
	GTATAATCCT CTAGTACCCT AGTAGTCTAG TATCTCCCAT AACCCCCCTA TATTACATAT	360
25	AATATGAGTA AAATACAGAA TGACGITAGC GCATAATCTA AGGCTAAGGT TGCCTACACT	420
	AAGITAACGG GGGCCTTCTT ATCTTGCAGC TTGTCCTTCT AATCAATAGA ATTCGTTTTC	480
30	TTTTTCCACT ATTTGGTCCC TGGCAAACTG CGAGCCACCC CGCGTATCCT TAGCCTCTGA	540
	OSTICIOCICI TOGACATCAC CITICOTOCIC COOGRATCICI COOGRACIGG TICAACIGIA	600
35	COCTOOGTOC ATATTTAGTG TOCTCAAGGT TOCTGAAAAT AGATGCCAGC ACCTTGTCCA	660
	GATAIT	666
40	(2) INFORMATION FOR SEQ ID NO:1126:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 642 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1686RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1126:	
5	GATOCTICTOC GAGGICAAGA GITGTGTCAT GAATTAACTT CATTITIAGGA ACAAACTTGT	60
	CTAGOGITCC COCTACTAAT TOCTOCTOGA CTTTGAAATC CCAAAATTTG ACAGTCTTGT	120
10	CTOCOGRACOC AGTICACTAGO CTICTTOCCAT CACTAGTTAG GTOTARAGAC CAGATTOCAG	180
	COGRETIGIEC CICTICAATA TITTICTAGCA TAGIAGAAGA TECCAGATCA AATAGCIGAA	240
15	GITGGCCCCC TCTTGTACCC AGAATAACCA AGGCGCCACC TGGIAAAAAC TIACAGCATA	300
	AAGCATAGOC ACAGICAAGA TIGOOGATAC AAGITTIAGT CITGATGTTC CAGACCITTA	360
20	GETTICCATT TGAAGCAGIT GCTAGTAGCT TATCATCGCT ACTGATGTCT GCAGCACGTA	420
	GATCAGTOCT ATGCCCCGCC GATTCGATAC TATGCAATTT GATCGCAGTA GGCTGGAGCG	480
25	GITCCITCTT TITGIATOGG ATTGAGIAGT ACTCITATAGT GITGITTOCA GICGIGATCA	540
	CCAGITCCAA TITAGATOOG GTACAGACOG TCCATGAAGA TGCTTTTAGC TTAAATAGGG	600
30	ACCITACCAG TIGGAAAAGG AIGCAAAAGT AAGITCGCAT AC	642
	(2) INFORMATION FOR SEQ ID NO:1127:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 675 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1687RP	
50		

(xd) SEQUENCE DESCRIPTION: SEQ ID NO:1127:

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	GATCAGGACA GTAGCAGCTT GACTGAGTAT CAGCAGGAAA AGCCTAGCTA ATTGGCCGCA	60
5	GIACAATIAC AAGIACCIGI CIGACIACIT CITTITGIGG GATGCCATAT TITITIAGGAT	120
	GOCCIOCAAC GOCCCOGIGG GOOCGCCATC CAAATTIAIG GAGIIGAAGA GCIGIICAAT	180
10	GCCCTTTATC CCATCTGCAC CGTCTTTATC GCCGAACATG GCATGCAACT CTTCAAGCAT	240
	GATATOTICT TOCTOGTOCT CTGATCCOOC GITGTCGTOG TTTGCCCAGT CTTCGTAGGC	300
15	GCCATTICIG TAATGITGAA GCTGTTCTTT GTTCATCTTC AGACCCTCCG TCAGGAAATA	360
	TICASAGAAA TOGTOTICAC TAATATOTAC GOUTICACTO TOGAAAAATG TOOGAGOOTO	420
20	TTCATCCCCA GCTGAAGACC CCTGACCAGA AACATGCTCA TTGCTACCTT CATCGTCATC	480
	TITAATATUT GICAGGAAAG TUTOCAGOGA CAGGGOCAAG GCATOCATAG ACGCCTUTIT	540
25	GTCCGCAGTC GGTACCTCCG TAGTTAATTC AGTCGTACAG AACTCCACCG GGCGCTCTAG	600
	CIGITTIGIA TGIACCAGAG COCTTACTAG GICACCCTCT AACTTICCTT TGOGINCAGC	660
30	TGTCGTTAAC TGGCC	675
	(2) INFORMATION FOR SEQ ID NO:1128:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 655 base pairs (B) TYPE: mucleic acid	
	(C) STRANDELNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) CRIGINAL SOURCE:	
	(A) ORGANISM: PAG1687UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1128:	
55	GATCOGTTCC AGTITIGGCCA GCGGAAGCTG GCGGACGAGG CGGACATCTG GGCTCATAAC	60

	GOUTOUCATA ACGIACACTG GOUTGACCAA CAGATOCOGC TOOCAAAGGA GAAGATAGAA	120
5	GAGCAGAAAG AATACCCGGT GCAGGAGTTT GACAAAAAGC TGTATCATAG CAAGCCCGCA	180
	AGGTACTOGG ATATATTCTA TAAAAATAAC AAAGAAAACT TCTTCAAAGA CAGGAAGTOG	240
10	TIGCAGATIG AGTITCCCTC TCTATACGAA GCTACCAAGA AAGATGCTGG TTCAGTGACT	300
	ATCTTOGAGA TTGGGTGTGG TGCGGGCAAT ACCATGTTCC CGATCTTATC TGCAAACGAA	360
15	AACGAACACT TACGCGTTGT GOGTGCOGGAC TTCTCCCCCGA AGGCCGTGGA ATTGGTAAAG	420
	ACGTCGCAAA ACTITIAACOC COCGAATOCC CACGCGACGG TATGGGGACTT AGCCAACOCT	480
20	CATGGTCTTT TGCCCCATGG TGTCCAGCCG CATTCGGTCG ACATCGCAGT AATGATTTTT	540
	GTTTTTAGIG CCTTGGCGCC CTCACAGIGG GCCCAGOCTA TGGATAATTT GCACAAAGIT	600
25	CTAAAACCAG GCGGTAAGAT CCTCTTTAGA GACTATGGCA GGTATGACTT GGCTC	655
	(2) INFORMATION FOR SEQ ID NO:1129:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1688RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1129:	
50	GATCTTGTTG AGAACACTCA ACATCCCCGT AATTCCAGAG CCCCCGGTGA CCATACCGAT	60
	TITCTTGTAC GCATTCGTCA CATAGCTGAA COGTOCTACA GGACCTTTGA ATTCCACAGT	120
55	TIGGCCTGGC TGTAGCCCAG CAAACCATTT GGATACCTTA CCGTCGACAT AAGATTTGAC	180

	MATCHIATCO MANICOCCCT COSCAMATTE GITCOAGAIM COCGIGIAGE MACCACITC	240
5	TTCTACACCA TCCAGCATCA CCTTCGCAGC TAAATGAAAG CCAGTAGGTA TATCAAGAGT	300
	TTCCACGCTT GAACGCAGCT TGAATCTGTA TATCGCAGCA TITTTTGCTTA GAACGATCCG	360
10	TTCTTCCAAT TCTAATOGCG TCCACTCATT TGGAAGAATT GAAGTCCTGC TTCTGTATGC	420
	TAGTAGCAGG OGTOCACCTA CAAACATTOC CAAAGCTAGA ATGCCTAGAA GGTACCATGC	480
15	GITCCCCCCT GACCAGOCGA TAACAAGAAC GCCCAATGTA AAGATGCCGC TGOGGATGAA	540
	GATCCCATGA ATGGGATCAT CCAATATCTC CATACCTCTG OGTTCGGTCA TACTAATATT	600
20	TTGAAAGCTC GTOGTAGCTA TOGTCTAGTA AGGATGAGAA COGTTAATAT ATGCTTCCTC	660
	CTAGTTCTAT AAGCACOGAC TOCTTTOCAA CTOGTGAAGT ATOGTCTAAC OGTCAT	716
25	(2) INFORMATION FOR SEQ ID NO:1130:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 676 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOLOGY: linear	
	(5) 10102001. 222002	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1688UP	
40	(S) CASALLET. FASTOGOF	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1130:	
	GATCAGGCCG GACCCGTACT TOCAGGAAAGC CCTCACGAAA CCCAAGGCCG GCGAGCAGG	60
50	CTTCTCGAGG TTTTTCAACG AGACGGGCTC GGGCAAGTTC GTGCCGCGGG CGGTGTACGT	120
	CCACTICCAC COCAACCICA TOCACCACCI COCCACCCCC COCIACOCC ACTICITOCA	180
55	CCCCCAGCAG TICATCAGCG CAAAGCAGGA CGCCGGGGAAC AACTAGGGGC GTGGGCACTA	240

	CACCCTGCCC CCCCACCTCT TCCACGATAT CCTAGACCCC ATCCCCAAGA TCTCCGACCA	300
5	GIGOGACGGG CTCCAGGGCT TOCTCTTCAC GCACTCGCTT GGCGGTGGTA CGGGCTCCGG	360
	CTTGGGGTCT CTGCTTTTGG AGCAGCTTTC TATCGACTAC GGCAAGAAAT CGAAGTTGGA	420
10	GITTOCCGTG TATCCCGCGC CACAGGTGTC CACCTCGGTC GTGGAGCCAT ACAACACCGT	480
	CITICACCACC CACACCACAT TOGAGCATICC CGACTIGIACG TTCATGGTCG ACAACGAGGC	540
15	CATCTACGAG ATGTGCAAGA AGAACTTGGA CATCTOGAGA CCTAGCTTTG CGAACTTGAA	600
	CAACTIGATO GOCCACGIOG TOTOCTOGGI GACOGOGICA TIGOGITIOG ACGCTOCIT	660
20	GAACGTGGAC TTGAAC	67 6
	(2) INFORMATION FOR SEQ ID NO:1131:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 700 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(ai) ODICIDAL COMPOR-	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI689RP	
	(A) Ordanism: Prescoore	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1131:	
4 5	GATCGIGCAC AAGITTICACG AGCTAAAGCT AAAGGAGGIG TIGITICAGAG GIAICIACOG	60
	THATGETTIC GITGACCCAT CIGCCATCCA CCASCETCCC ATCITGCCTA TCATTGAGGG	120
50	CCACGACGIT TIGSCGCAGG CCCAGTCCGG TACCGGTAAG ACTGGTACCT TCTCGATTGC	180
	TOCOTTOCAG AGAATOGACO AGAGCATCAA GOCCCCACAG GOGTTGATOC TAGCTCCTAC	240
55	CASAGAGTIG GCGCTACAGA TCCAGAAGGT TGTGATGGCG CTTGCCGCTGC ACATGGACGT	300

	TAAGGICCAC GCTTGTATCG GTGGTACGCA CCCTCGTCAG GACGCCGAGG CCTTCAGAGC	360
5	COGIOCOCAG ATTOTOGTOG GIACCOCCOG COGTIGUITTO GACATGATTIG AGAGACGIWA	420
	CITCAAGACT GACCACATCA AGATGITCAT CCTGGACGAA GCCGACGAGA TGTTGTCCTC	480
10	CCCCTTCCAG CACCAAATTT ACAAGAITTT CACCATGTTG CCACCAACCA CCCAGGTCGT	540
	CCTATTUTCT COCACCATCC CAAACCACCT CTTCCACCTC ACCCACAACT TCATCAACAA	600
15	GCCCGTCCAG AATCTTGGTC AAGAAAGCAT GCCTTGACCT TGGGAGGGTA TGCAGCAGTA	660
	CTATATTAAC GTOGAGAGOG AAGAGTACAA GTACGACTGT	700
20	(2) INFORMATION FOR SEQ ID NO:1132:	
25	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 657 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear 	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(ví) ORIGINAL SOURCE: (A) ORGANISM: PAG1689UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1132:	
	GATCOCOCTO AACCTCAGCO AGGCACGGCT GGTGATCAAG GAGGCGCTGC AGCACCGGCG	60
45	GCGGGTGTTC GGGCAGTGGC GGGACGGGCT GGAGGAGGAC GAGGGGGAACACA	120
	ATATGACGCA GGAGAAGGAG CTGGCGATGC TGGACAAGCT GCTGGAGAAG ACGACGGGG	180
50	GACAGAACCA GGCGCTGAAG CAGACGATGG TGTACCTGAC GAACTTCGCG CGGTTCCGGG	240
	ACCAGEAGAC GETGACGOOG GTGACGCAGC TOCTGOOGTIC GACGGGACTG CACCCGTTCG	300
55	AGATTGCOCA GCTGGGGTGG CTGGGGTGGG AGGACGCGGA GGAAGCCAAG ACGCTGGTGC	360

	COMPACTIONS CHALANTATIC TOCCACCHAGE ACCIOCAGGE CATCOTGAAG CACCIGIOCA	420
5	ACCIDENCAC CEIGINACTING ATMOCTINACAT AGRICAGGANG ARCITICOCCE CECCECCOCC	480
	CCACCAGTEG TOCACACAGE AGTECCATGT GTECTOCATG TOCACCECCT CECCECCCAA	540
10	CHICCACACE CACCOCTICCE CCACACOCCC CACCOCCCC CACCOCCACC TOCCCTACCC	600
	CACCTOGAAG TTACOGATCT COTOGAAGTG GTGCACCTOG TCCCCCCCA GGAACAC	657
15	(2) INFORMATION FOR SEQ ID NO:1133:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGIH: 718 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
25		
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) CRCANISM: PAG1690RP	
3 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1133:	
	GATCTGAAAC TAATGTCATC COOCGAAGAA CATACTAAGA GCTCATCGTT ACATCGAGAT	60
40	GAGACAAAGT ACCTGATGTA TAAGAGTTTT ATTGACATAT GCCCTCCCAG GCAAACGCCA	120
	GOCTACCOCC TGCCCCGTGT TCCGTCTACA CATGACAACA TAATTGTGGC AATGTCAGGC	180
45	GOOGIGGACT CITCAGTATG TOCTGCTTTA TACGCTCACT TCCCAAAAGT COGTGGGCTC	240
	TACATOCAGA ACTOGICOCA GACOTOGOCO TCAGGOCCTG TAGAGOGTAA GOCCGAACCT	300
50	TETTACEACC AAGATTOGAA GGATATTGAG AAAGTGGGCG CGTACCTTAA TATTCCCGTC	360
	GAGAGAGICA ATTIOGAACG GGACTACIGG CIGGATGITT TOGAGCCIAT GITACAACGG	420
55	TATCAACAGG GTTATACTCC GAACCCAGAT ATTGGCTGCA ACAGGTTTGT AAAGTTTGCA	480

	GUGITGUGG ACCACUTGGA CAAGGAGTAT GUACGGGCA ACTACTGGGT GGTAACAGGC	540
5	CACTATGGG GAATCCTATC COCCAGACT COCAGAGAGA COCAGGTGGT GCGGAGGGAT	60 0
	TATOCOCCAA AGGACCAAAG TTACTACTTA TCCCAAGTCC GGCGGGAGGC CCTCGCGGAC	660
10	CTCTTTAATG CCCATGGCAT TTCTTAACAAA ACCGCAAGTC CGACAATGGG CCGCAGAA	718
	(2) INFORMATION FOR SEQ ID NO:1134:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENCIH: 696 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) Original source:	
	(A) CRGANISM: PAG1690UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1134:	
35	GATCAGAAAC ATCACCATAT GGTGTCTGAA GACCTTACGG CGACGGTCGA TACACGCTAC	60
	CATCTCCAAG CCGATGATGC CGGCTATTAT GGACACCGCC GACGCCGTGA TTGCCAGGAT	120
40	TOSCASCITIC ASCASCITOSC TOCAGGIGAA OSTOCAGAAC ATOCCOGGICA GTOCCAGGIAC	180
	CACCITCACC GIGGTIGIGT TGTAGGACCC GAATACACAT GTGTAGTTGC TGTCCATGCA	240
45	CIGIATOTGA GACGOGCOCT CCATOTIGCA CGIGOGIGOG CTACACGICT AGCIGOCGCT	300
	COCACCIATA CTITICIATOT CTITICCCCCT TECTCCCCCC TACCCCCCTC CCCCTICCCT	360
50	CTTATCCCTT CICGAAGTCG TCTCCCCTAA GTTGGATCCC AGCGACCTCC TAGTCGAAAA	420
	CTGCTGTCTA CGTTCGCCAG GCACTAGTTG CCTCCCACTG CAGGTTATCG ATAAGTCCTA	480
55	AAATACCACC AAGCAGGCGT TGTACTGCTT CTATACGCCA ACCCTGGCTT TTCGTTGGGC	540

	TGACACACTC AAGTGACTGC AAGAACACTA COCTACTCAC AGATACOGTC GICOGTTGTA	600
5	COCACOCTAA AAGACAAGTT AAATCTACGA CACATATAGT GOCTOGCAAG CTCACOOCAT	660
	CCGGAAGGAA CAAGCTATTA GAAACTGAGA CACCTC	696
10	(2) INFORMATION FOR SEQ ID NO:1135:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 693 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1691RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1135:	
	CATCHICTT GIATTCTOGG TCTTACCTGC CCCAGACTCC CCTGTTACTA ACACCGACTG	60
35	GICCIOCCIC IGIGICAACA AGITOOGGIA IGOCIOCICC GCIACOGCAA AGATATOOGG	120
	CTOSTIGICT TOCTIGGGIG ACCOCATGGIA CAAGITCACA TAGIOCIGGG TGIACACUIT	180
40	CATGITGCIG TACGCATICA ACGCCACCAG GAATAGCCCA GAATAAGTAT ATATCATATC	240
	GICCITGIAT COGNICICCA AGNIGNACAA CACAGACOCC TOGNICAAGN COGNICAACIC	300
45	GCACATATOG TCTATCTTGT CAAACGTTGA CGCATTCACC GCCGGGGTCT CCACCTCCAG	360
	CACTICICGI TOUTIGCCAT TOACTOTOAC AAGACAGACC TICTCATCCT TGITCIGITT	420
50	GITTITAATT GICITTGIGG AAACCAACTG TOCITTCACA AACACCTOCT CASCATCIOG	480
	AACCCAAATC ATTIGACATT GITCACTCAT COOGACAGAT OCTOTIGAAC TTATCIAATA	540
55	TGCAATAACC AAATTCAACT TTACTTTAAT CACCTGCCTG TTACACACGA AGCAATGTTG	600

	GATCTCATAT TCACACCACC TACTTTTTG AAACACTTAT TIGTTTATGT COGOCTCGAG	660
5	CATACACCTC GCTCACCTCA CAAGCCCATG TAC	693
	(2) INFORMATION FOR SEQ ID NO:1136:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1691UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1136:	
30	GATCATTATG CAACOGAATC TOGTATCTCA GAAGATTACC GTAGGACTGT GOCTGTOCGA	60
30	TOGATTACGT TAGTGGGGTA GAGAATGAAG TAAGAAGCAG CTCTGCGAIT ATTGTCGCTT	120
35	TGCGCCTCAT GTGAGGTAAA GCCCTATCCC GCAGGGTGGC GGCTTTCTGC AAGAAAATCT	180
	GGGCATCACG CCCCCGAAAC GAAATGCGAT AGTCACCTGT GCCATGGCGA CGAGTCATTT	240
40	COCCATTOST ACAGAAATGA ACGGGCAGAA TOGCGTAATG GATTTTCTGT GGCGTTCGTG	300
	CCAAAAGGIG ATCTCCACCT GCGTGCTGCC CTGCGGGGGT GGTTGAGCAG AGCACCTGGA	360
45	AAAAGAACAG CACAGAAGOC CAATOCAGTT GOCCAATTIGA GOCAATAGCC GAGCAGGAAC	420
	AGTOCAAAGT GOGTGTTCIG GOOCTGTTGG ATCTGAAAAA TGCAGGAAGT TACAAAAAAAC	480
50	ACTOCOCCAA TACATACAAA CCOOCCGACCC GGCCATCCCC TAATCATCTG CCATCGACAC	540
	GCCGGGTCCCGG CCCTCGAACC AGCGGTCGAA ACCTTGAGGG CATGGTGATA CGCCCCCGTC	600
55	GGCGGGGCAC TCAAACAGGC ACGIGITAAT CCTGACAAAA CGCAGGGGG TAATTCCTTT	660

	CCCCAACCC GACCCCTATA TGAATCGTAC GATACCAGTT GTCGA	705
5	(2) INFORMATION FOR SEQ ID NO:1137:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 636 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1692RP	
20		
	(add environmentally environmentally environmentally	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1137:	
	GATCTAAATA TATATAATIT AAITTATAAA GATTAATATA AACTITITTA TTATAATATT	60
30	TAAGIATTAA ATTATTTAAA CTATTATTAT CATTATTTAA TAAATTAATT	120
	TAATACTTAT TATATAATTA TIATATAATT TACTIAATTC ATCATTATTA ATATTIATAT	180
	AATTATAAAA ATAATATITA ATATGAATAC TATTTAGICT ATGITCAAAT TTTAAATTAG	240
35	ANTINIUM VIUMITTA UNICENTA INTINOTOT MOTTANNE ITTANITA	210
	TIATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA	300
40	TAATIATT ATTATTTATT AATTOTTAT TAAAATA TATTITTATTA TATAAAAAT	360
	TEACTITATE TAAATATGE AAATTATTAT TETTATTAA ATATCIATEE TEATAAATAE	420
		400
45	TAIGHGAIT TAIATTATTT AAICHITHTA TAAGAATTAT TAHTAAAAIT AAITHTAACT	480
	TEASTETCET ATTACTATE TETATATAT TEASTANATE ATACTCATET TATETATETA	540
50	TITATTIAAT TAAATTAATT ATTTAATTAA TATTTATT	600
	ATATTATAAA GAATGTAGIT AAAAATACTT ATAAAA	636
55	(2) INFORMATION FOR SEQ ID NO:1138:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1692UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1138:	
	GATCTICATA CTAGAGCTIA TITTACTICA GCTACIATAA TIATICTIAT TCCTACIAGI	60
2 5	ATTAAAGTAT TTAGTTGATT ACTAACTATT TATGGTGGTT CATTAAGATT ACTAACACCA	120
	ATATTATATC TATTATCATT TTTATTTTTA TTTACTGIAG GIOGITTAAC TOGIGIAGIA	180
<i>30</i>	TRACCIAATO TATOATTAGA TETAGOATTO CATGATACTT ATTATETAGT ACTACATTTO	240
	CATTATGIAT TAAGITTAGG TOCIGIATIC TCIATGITIG CIGGITATIA TTAITGAAGI	300
35	CCTCTTGPTT TAGGITTAAA TIATAATGAA AAATTATCAC AAATTCAATT CTGATTAATT	360
	TTCTTAGGIC TTAATATTAT TTTCTTCCCT ATGCATTICT TAGGTATTAA TGGTATACCA	420
40	AGAAGAATIC CIGATTATOC TGATCTATIC CTAGGITGAA ATTTAGTATC TICATTTGGT	480
	TCTATAATAA CTATTATATC AITAAIGITA TTCCTTTATA TEATITIAIGA TCAATTAATA	540
45	AATGGTTTAA CIAATAAAGT TAATAATAAA TCIATTAATT ATATAAAACT ACCTGAITTIT	600
	ATTGAATCAA ATAATATTTC CITAATGAAT ACTACIAAAT CATCATCIAT TGAGTTTATA	660
50	TTAAATTCAC CACCICITAT TCATTCATTT AATACTCCIC TAATTCAATC TTAAAATAT	719
	(2) INFORMATION FOR SEQ ID NO:1139:	
55	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 714 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1693RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1139:	
20	GATCOCITIAG CGACTCTCTC CACCGCTCGA CGAGGCCATT GAGCTCTTAC GAACTGCACA	60
20	AACCIACIOG AACICIGITI CCAGACITCI TICTGITTGI CTICAACIGC TITCGCAIGA	120
25	AGTACCCCC AGGCTATTTT TCTTACCCCC CTGGTGTTTG TCTATATACC CGGTTGTATT	180
	TITIGATAAAA AACTCAGCTC TTOCTCTAGG GCAGAAATAT ATATOCAGTC CITAGCGCCA	240
30	TGCGAAAATC TGCCTTTTTA CCCCTGTTTC TCCCAGTCTT ACCACTGGCA GAAAAAAAGAT	300
	GTATGGGGTA TAGGGGGTGG CCCCCCCCGAA AAAAAAAAA AATAGAAAAA TAGAAAAATA	360
35	AAAAGACGTG GGCCGCCCCG CGGGCAGACG AAGAAAAAAT AGGCGCCCAC CCCTCCAAGC	420
	AGACGACAGG CGAGACATAA TAAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC	480
40	COGSCUTCAT ACSCUSCUAT TOTGTTCCAT COSSCUTUCA AACCCAGUAG TOGCATUTCA	540
	AAGCATTGCT CCCACCCTCC GCTGCCTTGC AGTGCACATC CTCTTCCTAA CCCCAGCCAG	600
45	ACTICCCATA CHITOSCACT TCACATAGCA TATCACTITT CAGATCACTT ACGICACATT	660
	CCGGTACCGA ATGGCACTICC AATGCCGACA AACCTCTTCC TACCCCGTGA CITA	714
50	(2) INFORMATION FOR SEQ ID NO:1140:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 692 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: single	

	TOSCOASCIC GSTTGTCGTC ACCCGCAGCA ACAGGACGAG AACTCTCCGC TTTCGGCCTC	180
5	GTGAGATTTT GGATTCAGTC ACGTGATTCA CGTAGAGGTT ACCCGGAAAG AGCCGCTTGG	240
	ATGCCAGTAA TCACCGCGT TATCCCCGGC CTTCTTAAGC ATTCAGTCTG AGCCGCTTCT	300
10	CCCCCCCTCC TIGITCICCT GGAATITCAA ACCCCCCCC GTATATACCC CCCCACAAAA	360
	ACACGGTGGC GAACGTTGTT GCCGCCAAGC GTTATCGTGA AGAACAAGCA TAATGGTTTC	420
15	CCCTTCGGTT ATTAAACAGG TGCAGGCGCT AATCCAGCAG AACCGCGTGT TCATTGCATC	480
	CAAGACGTAC TGTCCGTATT GCCAGGCGC AAAGCGTACG TTGCTGGAGG AGAAGCGCGT	540
20	CCCCGGCAAGC GCAGTAAAAC TGTTGCAGCT TGACACCATG GGCGAGGAGG GCGCGGTGAT	600
	CCAAGCGGCG TTGCAGGAGC TGAGCGGGCA GCGCACCGTG CCCAACATCT ACATCAACGG	660
25	GOGOCCATGIG GGTGGCAACA A	681
	(2) INFORMATION FOR SEQ ID NO:1147:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 667 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40		
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1698RP	
	(W) OUCHNITCH: NACTOROUG	
45		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:1147:	
50	CATCTOGTGC TTTTCAACGC GCCGCCCCAG ACAATTTCCG GAAGCATACA TATCGCCATT	60
	ACATAAACAG ATTITATGAC TAGTACAGIT AGGTATGTGG GAGATCACCG GAATAACTCC	120
55	TATATCTTAT TICTGTATTC TCAGGTACTG ATCGCTGTTG ATCAACGGC AACCCTGTGA	180

	CTTGCCCATT AACACTGTAT GAAGCCGGAC GGGGGGGTAG CACATTGGTA CTAGGCTGGC	240
5	TGAATTCATA ATTOGAATAA OGTOCTOCTT GCCCCCATGG CTOGTATGTC CGGTGCTGGG	300
	TIGAAGOCAT AAAATTOCTC GAGCIGTAGC ATGTTGCCTT CICTAGCATC ATGTTGTATG	360
10	TRACCIOCOC ATTORCCAGA ACCTOCOCCA ATGATGCAAG ATCTTCCTTC TTCTGCCCAT	420
	ATTIACOGAT GACTITICGIG ACATGIGGIC TAAGCGGTGT GACGGTAGAG TAAAGTTCIG	480
15	ATATCTOGIC TICGIGIGIC ACATCCACAT TOTGGGAGAC OCTTAGITTO TOGAGCAAGT	540
	TOTOGACATT GOOGGOTTIGO GCAAAGACAG CATGOTOCTG AGCAGOOTICO TITAGOTACOT	600
20	CCTCTGCAGT TGGCTCAGGG CATACGCCGA CATAATTICAC TGGGAAAAAT ACCAACCTTG	660
	CCGCGCA	667
25	(2) INFORMATION FOR SEQ ID NO:1148:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 572 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
<i>35</i>	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1698UP	
40	(A) CRISALIST: FASTOSOOF	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1148:	
	CATCACCAAG CTCCCCCCC CACCTCTCCA TCTCCCCCCC TCTACCTCCT TCTCCCCCTC	60
<i>50</i>	CTCCACTCAA CCATACATCT ACGGCTCTTA CAAGGGCATC CACATCATTG ATCTAAACCA	120
	CACCCTGTTT CACCTGAAGA GACCTGCGAA GGTCGTTGAG GGTGTTGCCG AGAATGGTGG	180
55	CCTGATCTTG TTTTTGGGTA CCAGAGAAGG GCAGAAACCA CCTTTACCCC GGGCTGCAGA	240

	CAGGGIGCGT GOCTGITATG TCGCCTCGAA ATGGATACCG GOGACCTTGA CAAACCCAAT	300
5	TGAAATATCC ACTIGTCTIGGG GCAGGCATGA AGTTGACTTC GAGGGCAATC CAACTGGCAG	360
	GGAATTGACA GAAGAAGAGA ACATCCGCAT CATAAAGCCG GACTTAATTA TIGITTIGAA	420
10	CCCAACAGAA AACATGAACG CGTTGAGAGA GGCTATGCAG GCTAGAGTGC CACCTATTGG	480
	GATCATTGAC ACCGACTICAG ACCCTTCAAT OCTCACATAC CCCCTCCCTG CTAACSAACG	540
15	ATTCOCTACG TTCTGTAAGT TTACTTGTAA AC	572
	(2) INFORMATION FOR SEQ ID NO:1149:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 664 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1699RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1149:	
40	GATCTOCCTG TATATTTOGA TGTATATOGA CITCACACTT TCOGAAGCAA TOGAACTOGA	60
	AAGCIGGIIG ACCACICIGC IGIATICIGG TAGICITICT GAAACGACGG TAAGAAAATT	120
45	AACCTIGAGC GGCGATAGGG AAGATGCAAC TITTAAATTTIC TICTACTTIGGT TACTICAAATTA	180
	CTGATATAAT AATGCAGCCT CAAATATGCT GTGGAAAACA CCACTTTOGC GGTTCGGAAC	240
50	ATTOGGTGGG ATTTCGATAA CCTGATTGGA GATCGGGAAC AAACTCGACG TAGTAGCCAG	300
	TAACGIGIAG CAAATATACT TTAAAACGIC GOCCTOOGC ACCATGITGC TGTAGTATGG	360
55	GITIAGACAGA TATOCCAATE GAGTATOGTE CTGCTGOGGC CGCTTGGGGA CCGGGCCCGCC	420

	(D) TOPOLOGI: TIMEST	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1693UP	
10		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1140:	
.5	CATCOGIAAC TICOGGATAA GGATIGOCIC TAAGGATOOG GIAGIGAGOG OCTIGGICAG	60
	ACCCCCCAAG TOTOCTTCTC GTCTCTCCTC GGGGGCTTGC TCCTGGGGAC GGACTGCTTG	120
20	OGTOCTOTOT OGTAGACOGO CTTOGTAGAC CATCTOTOGT OGTOCCTTOC TACAATTIAAC	180
45	GATCAACITA GAACIGGIAC GGACAAGGGG AATCIGACIG TCIAATTAAA ACATAGCATT	240
25	GCCATGGTCA GAAAGTCATG TTCACGCAAT GTCATTTCTG CCCAGTGCTC TGAATGTCAA	300
30	ASTGAAGAAA TTCAACCAAG COCOOGTAAA COCOOGGAGT AACTATGACT CTCTTAAGGT	360
	AGCCAAATGC CTCGTCATCT AATTAGTGAC GCGCATGAAT GGATTAACGA GATTCCCACT	420
3 5	GTCCCTATCT ACTATCTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGGGG	480
	GCAAAGAAGA COCTOTTGAG CTTGACTCTA GTTTGACATT GTGAAGAGAC ATAGAGGGTG	540
40	TAGAATAAGT GGGAGCITGG GGGCCAGTGA AATACCACTA CCITTATAGT TICTTTACTT	600
	ATTCAATTAA GOOGAGCTOG AATTCATTIT CCACCTICIA GCATTTAAAG TOCTATACOG	660
45	GCTGATCOOG GTTGAAGACA TTGTCAGGTG GG	692
	(2) INFORMATION FOR SEQ ID NO:1141:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 673 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOΙΩΤΥ: linear	

(ii) MOLECULE TYPE: INA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1694RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1141:	
15	GATCOGTTOC TTGAGAAGCA CCTAAAGCCT GAACTCCTGG CAGAAGCGAT CAAGGGAAACC	60
	TOTTGGGAGG GTAAAGITAG TATTAACTTG GTAGACGGAT TOGACCACTC GTATTACTTC	120
20	GTCAGCACGT TCGTGCCGGA ACACGCAAAG TACCATGCAG AAAAGTTGGG TCTAGTTTGA	180
	GATTIGACGI TOCOCCIGIT AAITOGIATA TACTTACATA TITAGICATA TGACGGCTIC	24
25	AAGIACTOTO ATTOTOCATT ATAAGTOCAG COGAATOCCA GOCTOCOGCA GTAATOGCAA	300
	COCAAACTGA ATTIOCOOGI AGITCAACCT TGOCOGGITG CAGCACOCGT ATGCTCCCAG	36
30	CAGACTCAAA CSTCGCTATT TGGCGGGTAT CTACAGCCTC GTGGGGATCT CCCTGCCCAA	42
	GACAGOCACA GATATCACTC TOCAGOCOCC AGGAGTAGAG TTCACCTTTG TOGGTTAGAG	48
35	CHAGGITGIG GIAGICTOCC GCAGATACAG CAATAAACTT CIGGOCTIGT TOCAAATTCA	54
	TOTTCATGAA TGAGTOCTOG ACGATATCAC CATTATTCAC CITCAGGGTG TATIGTGCTAT	60
40	TCTCGGTACA TAAAACCAGT GTCATGCAAG ATGCCTCAAT CTTCGTTAAC CGTCCCATCAA	66
	ATGGCAAAAT CAA	67
45	(2) INFORMATION FOR SEQ ID NO:1142:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 676 base pairs	
50	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(D) IVEVIXI. IMEDI	
55	(ii) MOLECULE TYPE: DNA (genamic)	

	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1694UP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1142:	
10	GATCAGCCCC CCACCGAAGA ACACTGGCTT CCCTGTGGGG AGGGCGGAAA TICTTGGACC	60
	GAGTATCAAC AAATOCAGIT AGATAACGAT CACATGATIG CAACACTGOG GGAATTCATT	120
15	AGITTACCAGA CTGTTTCCCA ACTCCCAGAG CCCCAAAATA TCATCGATTC GCGTAGGTGT	180
	GCCAACTTCC TCCAAAATCT CITCACTAAG CTCGGTGCTA ACCATTGTGG GCTTATACCT	240
20	GICAGIACAG GCAGCAACCC GGIGGTICTC GCGCAGITICA AGGGCAAITGC AGCGCGCCC	300
	AAACGCATAC TATGGTATGG CCACTACGAT GTGATATCCG CGGACCACCC GTGGCAGTGG	360
25	GACAACGACC CCTTCACGCT CACTTGCGAA AATGGGTATC TTAAGGGAAG AGGGGTGTCT	420
6.0	CATAACAAAG GOOOGCTGCT TGCCGCCCATC TTCAGTGTAG CCCAGCTTTT CCAGAAAGCA	480
30	TACCTGAACA ACGACATCAT CTTTCTAGTC GAGGGCAGG AAGAAAATGG CTCTCGCGGC	540
35	TICAGGGAAA TITTIGCITGC CICCGAAGGG CTICICAATC AGCGGIGGGA CIGGATCCIG	600
35	TTCAGCAATT CCTACTGGCT GCATCAGAAG GTGCCCTGCC TCAACTATGG CCTCCCAAGC	660
40	GTCATAAACG CCGAAA	676
	(2) INFORMATION FOR SEQ ID NO:1143:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 711 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1695RP

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	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 1143:	
5	GATCTGCCCC CAAAACAITT CGGTGCCGGC TACCCCAAAA GATTTTGGGT GCGGGCTACC	60
	CCATCACGAG ATGGCACTGG CTCATTGGCG AGCTCCTGGG CATTTGCCTA TGACACAGAGA	120
10	ATGAGTCAGC TITACTCCGC CACACCATAC TCCCGGGCCT TCAACAAGCT TCTGTTTGCC	180
	ATCESCATOG TESCCAGTTC TTACACTECE CCCCACCTG CATCESCAGCC	240
15	GITTIGICAC AGITICICCCI COGCAGGIAT CGICTOCGCA COGGIAACGG ACGCGACTAC	300
	SCASOSSCIE COSCACTCAC GISCOSSOSS GICTICICIC CCACOGIGAT AGICACTITI	360
20	CASTASTSTS TOCTOCCTTG AATTOGCAGG GCAATOSTTC AASCTGCTCT GGCGCGGACG	420
	ACGACCOCAT CTCCGCAACG GCGTTGGCGG AGAAAGGGTG TTTCGCGACCA GACAITCGGCC	480
25	ATCHOCOGCA GICAGCAGCT GCCTTGGEAC GGAGCTACCT GICTATATTA TCCCCTTAAT	540
30	AAACATIOGA TATGCCIGIT ATTGTATGCC AACGGTTCTC CGGGTACAAC GGGGTAGTCC	600
30	OSCOCCIOCO TGAGCIATOC TOSCOGATGI GAAGTOCCIT TOGITAAGIG GICTOCTTIC	66
35	CCGGGCCACT TGTAAACACT ATGGCGGATC ATACAGCCAG GACTCAAATA C	71
	(2) INFORMATION FOR SEQ ID NO:1144:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGIH: 654 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ODCANTOM, DACI COSTO	

(A) ORGANISM: PAG1695UP

55

(xi)	SECUENCE	DESCRIPTION:	SEO	\mathbf{I}	NO:1144:
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5	CATCTGAAAA GCACGAAGTC GCAGTGGGAG GCCCCTGCGG GCACGTGGTG GCCAGCGAAG	60
	GETTOCOCCUE ACCICICACC GECGTACCAC ACCICCOTTCG CACCOCCCCC CGCGCACCGC	120
10	GOCCAGGOCG TTGCCCCCCA GOCCGACTAL GGCALACAGG CCGCATALGGC GCCCCAGGGG	180
	TACOSCOCC GOCCOCOTA CACGOCCCAG COCCGCTIACG GCCCACAGCC CGGCTIACGGC	240
15	ACACAGOCOG GCTACOGTOC ACAGOCOGGC TACOGGOGCAC AGCCCGGCTA COGGGCCACAG	300
	CCCCCCIATG CCCCCCAACC CCGTTACGCA TACCCCCCCC AGCCCCCCTA TGGTGCCCCC	360
20	CCCCCCCCCACCA CCCCCCCCACCAC GCTTACCCCCC CCGCCCCCACC CCCCCCCCCC	420
	CAGAACESCG GCCGCAACAA CATGATGATG GSCCCCTGA TGGGTGCCGG CGTGGGGTTG	480
25	ATGGCCGGGT CACTAATGAC CACAGCCATG TATAACCACG ACAAGGACGT GGCCGATGCT	540
	SCCTACGACC SCSSCTATGA AGACSCTTCA TOGACSSCGA CITICTAGSCC GCACCCCGTC	600
30	ACGTGCCAGA CCCGTAGAGA GCTAGGACAA CITACGTAAC GCGTCGACGT ACGC	654
	(2) INFORMATION FOR SEQ ID NO:1145:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 711 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1696RP	
5 0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1145:	
	CAMERTICATIVA MACAMINICA CA MACAMANATI MICAMANA A AMAMANATIVA MAAMAAAAA	CD

	COCCAATCICG GICTACGATC CCCCCCGAGAA CGAGGACACG CTCCTCCCCC ACTTCCCGCAC	120
5	GRACCACCIC TGICCIGAGG AGICTCICOG GTIGATAAAC AAGCGGITTG TTCCGAATCA	180
	CAAATOOGAG TITICTCCATG GTGAAACCAT GGTAATOCCG CTCTCCGAGT GCGTTGAGTT	240
10	CATTAACOGG CITTATCGAGT ACTACCTGTA CCCACCCAGG GGGGTGGAGG ACAAGTACTC	300
	GCGGGCAATT GTGGGTCATG GTGTCTCTGG TGATCTGCAA TGGCTTAGGA GTCTGCTCAT	360
15	CCACCIGCCC ACGATCGCTG GCCCAGGCAA CTCCCCATCCG CGCCACCATG TTTCTGTCCT	420
	ACATACOGOG CATITIATACO AGIACITICTA TOGICAGAAG GGITICATOCO TAGGITAGAG	480
20	CTTAAGATTG CACGGTGTCC CACATAGCTA TCTGCACAAT GCAGGCAACG ATGCATATTA	540
	CACATTACAA CIGCTCATGA AGATGGGGGA TGTGCAGCAA CGCATGGGG ACCAATGGGA	600
25	CCATCTATAT GCTGTCTTCC ACACGTTGAA GCAATGGGAA GAGTATGAGA ACTCCACGCC	660
	CTOCACTORG CACOCAGAAT COGTOCATAA CAGCACOCOC OCTACOORGA A	711
30	(2) INFORMATION FOR SEQ ID NO:1146:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 681 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) Original Source: (A) Organism: Pag1696UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1146:	
	GATCOGTCAG AAACCCATCG CCTCGCTCGC TCGTCTGCTA ACGCCCAGAA CGCCACCTGT	60
55	OSTICTITICA CTOCCOCTOS TICCTTATIC COCCACOGGS (CTCGTGGGS CCGCCAGCGC	120

TOSCONSORE GETTOTOGTE MOCESCHOCK MENGGACING AMETETOCOGE TETTOGGOCTE	180
GICAGATTIT CCATTCAGIC ACCICATICA COTAGAGOIT ACCOSGAAG ACCOSCITICO	240
AUGCCASTAA TCACCCCCST TATCCCCCCC CTTCTTAAGC AFTCACTCTG ACCCCCTTCT	300
COCCECTICC TIGHTCHCCT CGAATTICAA ACCGOGGGG CTATATAGGC CCCCAGAAAA	360
ACACCISTOSE GAACISTICIT COOSCEANCE GIVATOSTICA MICHACIACOA TRATEGITITE	420
COUTTOGGTT ATTANACHOG TOCHODOGT ANTOCHOONG ANDODOGTGT TUNTTOCHTC	480
CANCHOSTAC TOTOCCSTATT GOUAGGOOG ANAGOSTAGS TRUCTOGROS AGANGOSCST	540
COCCECNACE GUAGIAAAAC TOTTGGAGET TGACACUATG GCCCCAGGAGG GCCCCCCCAT	600
CCANGEERE TTOCKGENEC TENECOSICA GESCACOSTG CECANCATET ACATEMACIA	660
GESCHATOTO GOTGOCHACA A	681
(2) INFORMATION FOR SEQ ID NO:1147:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 667 base pairs	
(B) TYPS: nucleic acid	
(C) STRANCEDNESS: single	
(D) TOPOLOGY: Linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:	
(A) CPGANTSM: PAGL698RP	
(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:1147:	
CATCIGGIGC TITTICAACGC GCCGCCCCAC ACMATTICCC CAAGCATACA TATCCCCATT	60
ACATIAAACAG ATTTTATGAC TAGTACAGTT ACCIATOTOG CAGATOAOOG GAATAACTOC	120
DATABELIAT TENGIATIC TEAGGIACTG AIGMENTING AIGMANNING AACCEGIGA	180

	areasons whereas areasons ever last contains	#4U
5	TCANTICATA ATTOCANIAN GETGCTGCTT GOODGATGC CTGGTATGTC CCCTGCTGGG	300
	TIGARGUAT AARATIOCIC GAGCIGINGC AIGITOCCTT CICINGCAIC AIGITOINIG	360
10	TARCCTOUGE ATTOCCOACA ACCTUGUICA ATCATOCAAG ATCTTOCTTC TTCTCCCAT	420
	ATTIPACECAT CACTITICATE ACATETICATE TRACCOCATE GACCOTACAG TRAACTICATE	480
15	ATATCICUSIC TROOTGICIC ACATCCACAT TOTOGGAGAC COTTAGITTO TOGACCAAGT	540
	TOTOGRACKIT COORSCITCO CONANGNONG CATOCTOCTO MOCACCOTOC TINGCINCOT	600
20	COTOTOCAGE TROCTOROGO CATACOCCOA CATALETICAC TROCALALAS ACCIACOTTO	660
	CDBCDCN	667
25	(2) INFORMATION FOR SEQ ID NO:1148:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 572 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDRINESS: single	
	(D) TOFOLOGY: Linear	
	tol see months of the see	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(v1) ORIGINAL SOURCE:	
	(A) OPCANISM: PACI 698UP	
40		
45	(sd.) SEQUENCE DESCRIPTION: SEQ ID NO:1148:	
	CATCHOLAGE CTOCCCCCC CAGGIGIGCA TCTOCCCCA TCTACGICGT TGTGGGGGCTC	60
50	CICCACICAL COMPACNICI ACCICITA CAAGOOCATO CACATONITO ATCINAACCA.	120
	CACUCTOTTT CACCTCAACA CACCTOCGAA CGTCGTTCAC CGTGTTGCGG ACAATGGTGG	180
55	CONCADOTTO TOTTITICACIDA COMPACAMACIA CONTRACISCO GEOGRACIA	240

5 TCHAMINTOE ACTICICIOGG GENGGENTGA ACTICACTIC GAGGENATE CANCIGOCAG	
5 TCHANTATOL ACTOROGOG GENERICA AGPICACITE GARBONATE CANCIONOS	360
CCANTICACA CAACAACACA ACATOLISCAT CATAMAGOIG CACTINATIA TIOTITICAA	420
OCCANONGRA ARCATGAROG COTTURCINO GOCTROTOCHO COTREMOTOC CACCURITIES	480
GATCATTCAC ACCURACICAG ACCUTTCAAT GUICACATAC COURTCOCTG GTAACSAACG	540
ATTOCCIACS TICTGIRASI TEACTIGIAA AC	572
(2) INFORMATION FOR SEQ ID NO:1149:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 664 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: Linear	
(ii) MULECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:	
(A) CRCANISM: PAG1699RP	
35	
(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1149:	
GATCHOOSIG THEATTIGGA TERATHINGA CITCACACIT TOSCANOCAA TEGAACTOG	A 60
AAGCTOGTIG ACCACICIOC TOTATICIOG TAGICITICI GAAACEACOG TAACAAAA	T 120
ANCESTERIC GOCCATACOS ANGAIGCANO TERNANTEIO DEDICTIGOS ENCICAANO	A 180
45 CIGATATRAT AATOCAGOOT CARATATOOT GIRGAAAACA CONCITTOOC OSTITOGAA	C 240
ATTOROGO ATTOCATAA COTGATTOGA GATOGOGAAC AAACTOGACG TAGTAGOCA	va 300
TANCHUM CHARITETHET THANACCIC COOCTCOSCC ACCUTOTICS TOTAGIRE	360
TWENTALL COLUMNS THE SENSE PROPERTY IN THE SENSE	

	GTAGGCAGAG GTTACCGCCG ACCGGCGCTC TGAAAGCCCC TCCACATTCT CGAACGACTC	480
5	TOCATACACA CITAACCOCCC TCGACGGCGT CATCAGCGAG TIGTGCCGTT GCAGCGTGCC	540
10	CTTCCTAACA TATCCACACG COGTGCCCCT GTGTCCCAAG CCCGTCCTCT CCTGCCCCAC	600
	SCHEFFICAGE ACCERCAGET ACTICAGGAC CIGCICCITE CIACOGAAAC ICTCCAGCAC	660
15	TITIC	664
	(2) INFORMATION FOR SEQ ID NO:1150:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 642 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1699UP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1150:	
	GATCTCCACC GCGTCCAGCA CCACGATCGG GTCACCGTCC CACGGCGTCA TCGCCACTGT	60
40	CONCONCRACE CITICGAAAA CONCONTRIC CICONNOCTC OCANOCOCTC COCONNICT	120
	CTCCCTCCCC TCCTCCCCCT CCCCCCACCC CAGCCTCCCC ACCACCCCCT CTATATTCAC	180
45	GCCCCCCCCCC TTCAGCCTICT CCCCCCTTCAT GCCAGCCCTG GTGCGTTTCT CTCCCACCAC	240
	CTCCAGGCTC TTGATAAACG TCGTCTTAAT CACCTTAAAG CTCGCAGTAT GGCCCTTGCG	300
50	COCACATAGT AGOGTCAGOG TATOGTTTOC CGAATOGTAC GOGTATATICT TOCCCTGTGT	360
	TACACOGICG AGGACGITGG TCACCOGCAC CITGAATCCA AGGATATGIT CCAAGTIGAT	420
55	OCTICATTICTG CTCACTTOCA AGOCCACACA GCTATOCTOG CCACCTTAGA ATGCCACOCC	480

	TOCTOCOCCT OCACTOCCIC ACTOCCAATC GITCAGTTIG COGIGIOGGT ATTITITITICA	540
5	AGTOCCCCC TAACCATCAA GTACCATTIT CTATGTATTA CTATGTCCCA CAAACGTTAG	600
	TITCCAATAGT GCTTGCAACT ATCAGGTGCT GTGGAATTCC AA	642
10	(2) INFORMATION FOR SEQ ID NO:1151:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 624 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1700RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1151:	
	GATCAGCAAC COCAGCGCAT GAGGCAGTCC GCTCACGCAC GGTCTTGTTT TCAGCGCTTG	60
35	GCTTGCTTTT CICCTTTAIG CGTTGTACIA CTTCTGTGAT GTGCTCGGCA TCCAGGCCCC	120
	TITICCITAG CCIGCITOGI AACCIGCGCA GGCGGCGGIT GCTACGAACA CGCAACITGG	180
40	CITICIOCATO ASCAMOCTOS GOTOGOTOTT TOCOCADOCO TIGOCATOCT COCOCATOCT	240
	COCGUTCAAT ATACCAGAAT OCATCATOCT TOOCTOOCTC TATATTGACC TOGTOOCCAT	300
45	ATATCAAAAG GCGGTCCTTG AAGTTTTGTA AAAACTCGTC TGCCTGAGAT GGCGTAGCGA	360
	ACCCAACCAA GCATTTATTG COOCATTTAC GAGGCCTGCA AACACTAACT ACCCCTACT	420
50	TOTOATOTAC CAGTOGAAGS COCACGTOTG COCAAGGAAG COOCTOTOGC AACGTTTTCT	480
	CCGCCGATAG ACCATATOCC TTATCCTIGT TGATGGACTT CAACAGTIGT CGAGCATATT	540
55	CTATCCTOGA GOCATTIGAC GCTGGCAAAT TTGACAGGTA GACACTGGAT GGCGGGGTTA	600

	GTATOGAATC GACAGCAGTA TAGC	624
5	(2) Thisponagues for the re-	
	(2) INFORMATION FOR SEQ ID NO:1152:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 603 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1700UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1152:	
	CATCACTOSC CCTGCAGGG CGCGCCTTT TGCGGCTGTT GTAGAACAGC ATGCCGCGGC	60
30	GGACCTTGTC ATAGAAGTGT TTAGACTGTA GGGTTCCCAT CGAATGGGAG CGGCGGTAGC	120
	TETCACTTIT CATCATAATC COOGIOCANA OCTTCAOGIG GICCTOCTAC COOCAGCAAA	180
35	TEAGETTECE COOCACACEA SEGIOGICOS COOCOCOCAS CEACEACOCO COCCATOCOC	240
N _	ACTICCAGGA CITOCOCCAC GACGOCGOGT GOCGCGAGGA GIAGGAGGGG ATGCCGGAAGT	300
40	CCCCCCAAC CTGCCACCCC CCCACCCACC ACGTGACCCC CTTCAANAAA CCCCCACCCC	360
45	GETTGGCGGG CTGCAGCTGG CCGGCGACAA ACGCAGAGCC GCTGTGGGCG AGACCGGTGG	420
45	GOOCOCCTOC OCTOCTOCTA ACCCCACTOG COGACTCAGG CAAGOOGGAC ATGCCCCOGA	480
50	ASTAGEGECC GETGITGGCG CTGAGETTCG GAAACATETT GGAGAAGAAG COCCGCTCCG	540
	TEGRACIONA CACOCOGTICO COCTIGGAÇA TETECTOCTO COTOGRAGIOS COCCAACTOCT	600
££	CCA	603